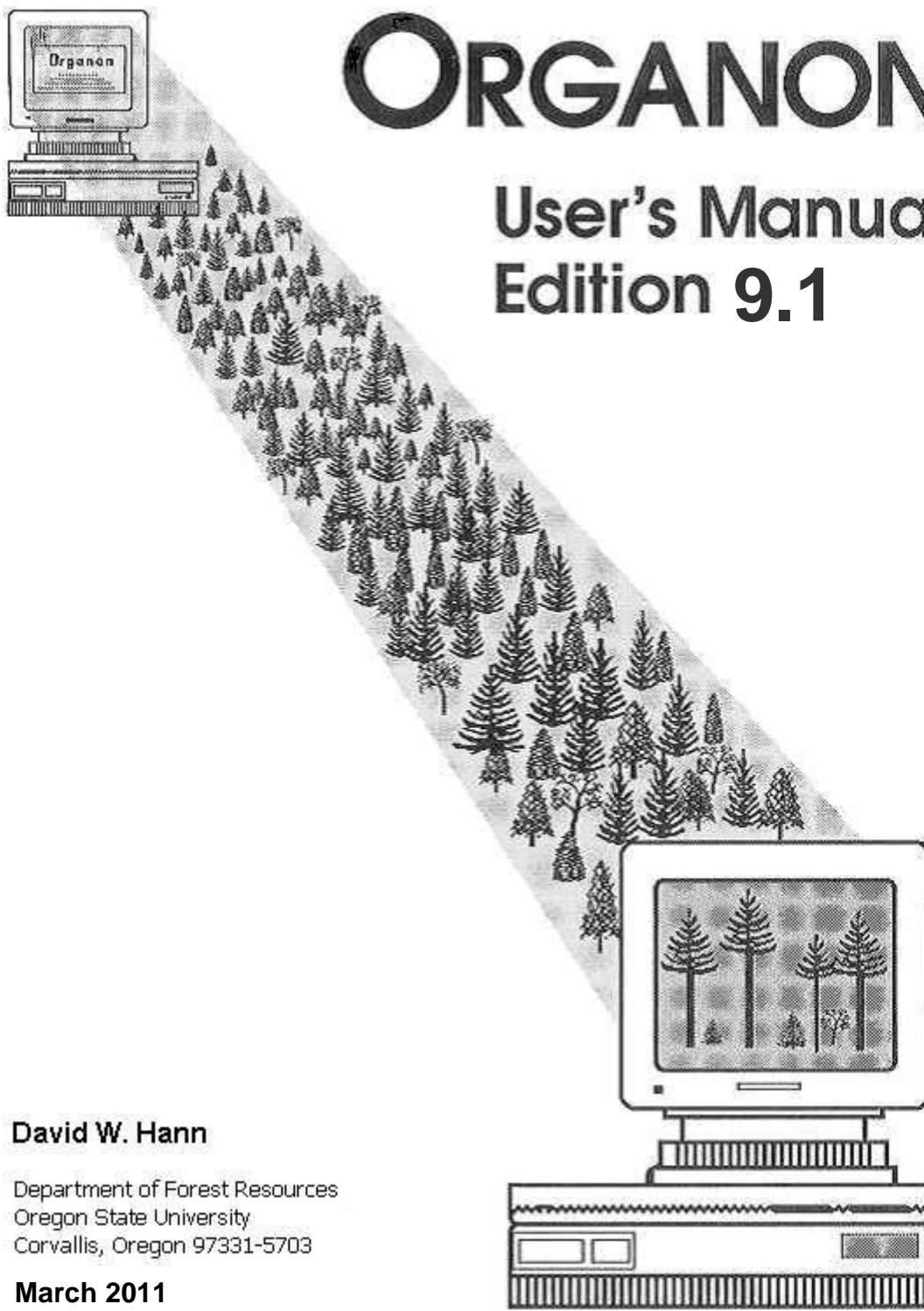


# ORGANON

## User's Manual Edition 9.1



**David W. Hann**

Department of Forest Resources  
Oregon State University  
Corvallis, Oregon 97331-5703

**March 2011**

## **The Author**

David W. Hann is professor of forest biometrics Department of Forest Engineering, Resources, and Management, College of Forestry, Oregon State University, Corvallis, 97331.

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## I. INTRODUCTION

This user's manual describes how to operate the ORGANON (OREgon Growth ANalysis and projection) growth and yield model. Currently, the program incorporates three versions of ORGANON: the southwest Oregon version (SWO-ORGANON), the northwest Oregon version (NWO-ORGANON), and the Stand Management Cooperative version (SMC-ORGANON). While all of the examples presented in this manual use SWO-ORGANON, the manual is intended as a reference for all versions. Where appropriate, differences between the three versions will be noted in the manual.

SWO-ORGANON has been designed to project the changes that take place in the mixed species forest stands of southwest Oregon. The major conifer species in such stands are Douglas-fir (*Pseudotsuga menziesii* [Mirb.] Franco), grand fir (*Abies grandis* [Dougl. ex D. Don] Lindl.), white fir (*Abies concolor* [Gord. & Glend.] Lindl.), ponderosa pine (*Pinus ponderosa* Dougl. ex Laws.), sugar pine (*Pinus lambertiana* Dougl.), and incense-cedar (*Calocedrus decurrens* Torr.), either singularly or in combination, and the major hardwood species are Pacific madrone (*Arbutus menziesii* Pursh.) and golden chinkapin (*Castanopsis chrysophylla* [Dougl.] A. DC.). SWO-ORGANON can predict both even-aged and uneven-aged stand development, starting from the time when the trees in the stand are no longer being affected by non-tree competing vegetation.

NWO-ORGANON has been designed to project the changes that take place in the young-growth, Douglas-fir and western hemlock (*Tsuga heterophylla* (Raf.) Sarg.) stands, either singularly or in combination, of northwest Oregon. While NWO-ORGANON can predict the development of even-aged and uneven-aged stands, most of the data that was used to develop the model came from even-aged stands with ages ranging from 10 to 120 years old, as measured at breast height.

SMC-ORGANON has been designed to project the changes that take place in the young-growth, Douglas-fir and western hemlock stands, either singularly or in combination, of southwest British Columbia, western Washington and northwest Oregon. While SMC-ORGANON can predict the development of even-aged and uneven-aged stands, most of the data that was used to develop the model came from even-aged stands with ages ranging from 1 to 80 years old, as measured at breast height.

RAP-ORGANON has been designed to project the changes that take place in the young red alder plantations of western Washington and northwest Oregon. All of the data that was used to develop the model came from even-aged plantation with ages ranging from 3 to 18 years old from seed.

ORGANON is an interactive program written in standard FORTRAN 77 code designed specifically to run on an IBM PC or compatible personal computer. The program is "user friendly" and should guide users through its execution. The user manual should help you prepare the tree data input file as well as run the model.

## **A. *What you Need to Know to Use ORGANON***

ORGANON users should have a fundamental knowledge of Windows, including simple file management (printing, name restrictions, etc.), keyboard familiarity, and disk management (default drive, file drive specification and path names if using hard disk subdirectories).

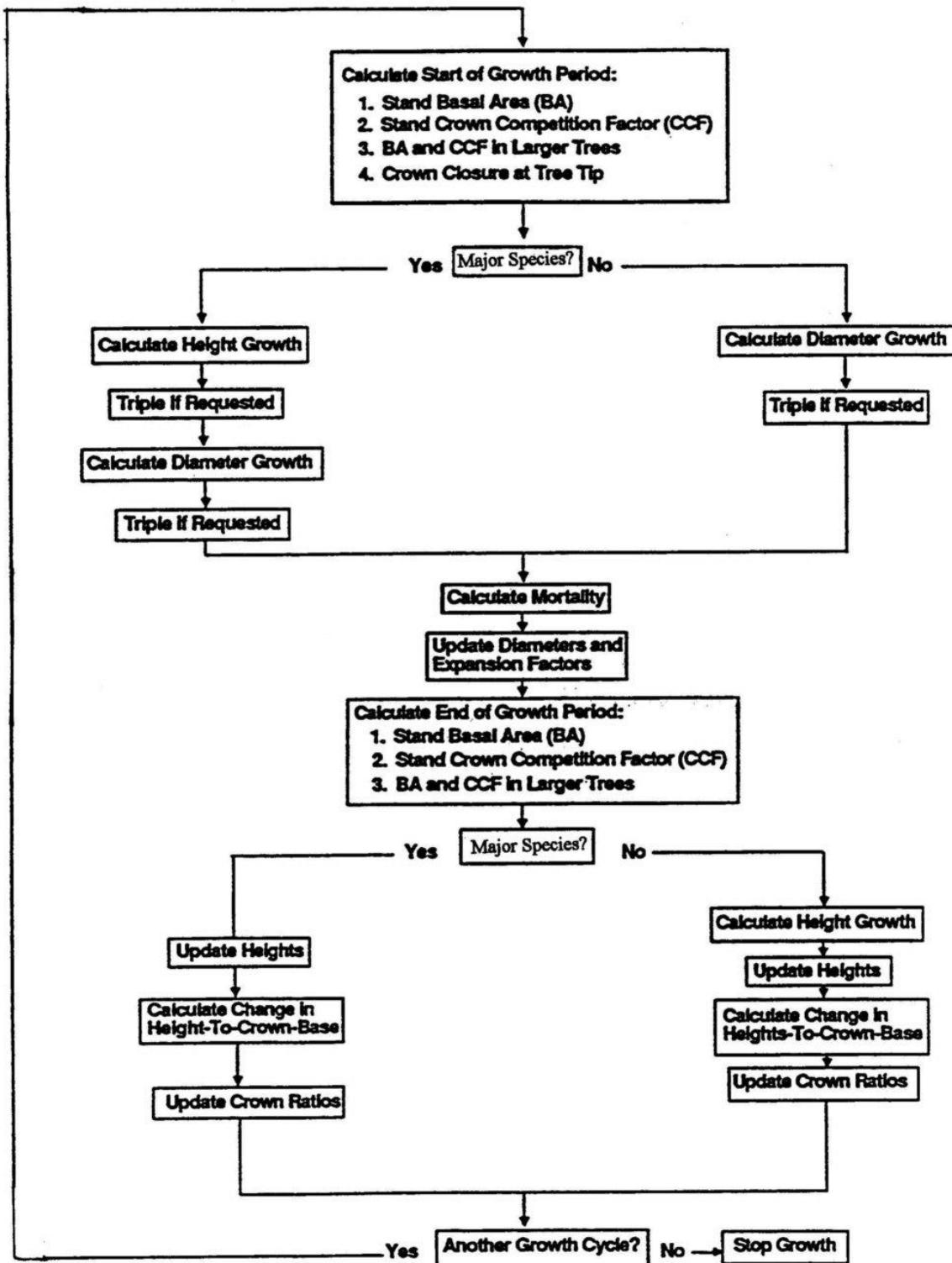
You should realize that computers distinguish the difference between 0 (zero) and O (oh) and 1 (one) versus l (lower case letter L). Please be careful to enter the correct values.

The use of '<CR>' in this manual and on the computer screen during program execution refers to using the key marked 'enter' or a bent left arrow (depending on the keyboard). Pressing the enter key, depending on the situation, restarts a suspended operation of the program. Otherwise, pressing the enter key selects a default response designated by parentheses in the request (see Execution Suggestions). This manual designates all user input by printing those responses in bold type.

## **B. *Overview of the ORGANON System***

The following illustration depicts the entire ORGANON system, showing each of its major components and their relationship to each other.

## GROWTH CYCLE FLOW CHART



### **C. How to Report a Problem**

Any problems with running ORGANON should be reported either by E-MAIL to [DAVID.HANN@OREGONSTATE.EDU](mailto:DAVID.HANN@OREGONSTATE.EDU) or by mail to the address listed on the cover. It would be helpful if you could provide the following information:

1. The version and edition of ORGANON that is giving the problem.
2. A brief description of the problem.
3. If available, either an E-MAIL attachment or a printed copy of the output file, including the run history.
4. Either an E-MAIL attachment(s) or a computer disk/CD with a copy of all appropriate data files (such as the initial data input file, the .INP file, the wood quality output file, the tree list output file, and/or the ingrowth file).

We would also like to hear of suggested changes for future editions of ORGANON.

## II. PROGRAM PARAMETERS

### A. *Logged Drive*

The logged (or default) drive is the disk drive the system searches to find the data file name you typed in. If a file does not exist on the logged drive, you must enter a drive designator (i.e. B:) along with the file name. ORGANON then searches the correct directory for the file name designated. If the file is not found in that directory, an error message is displayed on the screen and you must re-enter a file name. For file name errors, be sure you have typed the correct drive designator.

### B. *File Names*

ORGANON accepts file names that follow Windows short file name convention. These consist of up to an 8 character name separated from a 3 character extension by a dot '.'. See **Filenames, Forbidden Characters** in file names in the help file of your Windows version for further information. After ORGANON reads the raw data file, additional variables are calculated and a new file with the same root name is created. The 3-letter suffix, or file name extension '.INP', is appended to the root file name (after any existing extension on the raw data file has been first removed). This file is written to the same drive from which the original data file was read.

### **III. ORGANON INPUT DATA**

The ORGANON model is designed to project the future development of existing stands. Therefore, ORGANON requires certain tree and stand information in order to operate. This information should come from a statistical sample of trees from the stand. A maximum of 2000 sample trees can be entered for each stand.

#### **A. Stand Data**

The two data elements that may be entered for each stand are:

- site index
- stand age
- planting density (RAP-ORGANON only)

#### **1. Site Index**

SWO-ORGANON requests two site indexes, Douglas-fir and Ponderosa Pine, based upon the equations of Hann and Scrivani (1987). You must enter at least one of the two site indexes. If both values are entered, both are used. If only one value is entered, the site index not entered is calculated from the entered site index.

NWO-ORGANON also requests two site indexes, Douglas-fir and Western Hemlock. You must enter at least one of the two site indexes. If both values are entered, both are used. If only one value is entered, the site index not entered is calculated from the entered site index. Douglas-fir site index is calculated from King's (1966) dominant height growth equation. Western hemlock site index is calculated from Flewelling's unpublished dominant height growth rate equation.

SMC-ORGANON also requests two site indexes, Douglas-fir and Western Hemlock. You must enter at least one of the two site indexes. If both values are entered, both are used. If only one value is entered, the site index not entered is calculated from the entered site index. Douglas-fir site index is calculated from Bruce's (1981) dominant height growth equation. Western hemlock site index is calculated from Flewelling's unpublished dominant height growth rate equation.

RAP-ORGANON also requests two site indexes, Red Alder and

Douglas-fir. You must enter the red alder site index. If both values are entered, both are used. If only the red alder value is entered, the site index for Douglas-fir is set to a value of 115-feet. Red alder site index is calculated from the Weiskittel et al. (2009) dominant height growth equations. Douglas-fir site index is calculated from Bruce's (1981) dominant height growth equation.

Guidelines for measuring and a site index calculator can be found in section IV.A. Site Index Calculator.

## **2. Stand Age**

If the stand is even-aged, then the stand's age must be supplied. For SWO, NWO, and SMC versions of ORGANON, the age is measured at breast height. For the RAP version of ORGANON, the age is the number of years since seed.

## **3. Planting Density**

The RAP version of ORGANON also requires the entry of the planting density used for the plantation.

## **B. Tree Data**

The eight data elements that may be entered for each tree in the stand are:

- plot/point number
- species code number
- diameter (outside bark) at breast height
- total tree height
- crown ratio
- expansion factor
- radial growth
- user code

### **1. Plot/Point Number**

A plot/point number is a unique integer between 1 and 999 for each sample plot/point. The number does not need to be consecutive or sequential. For plots/points with no trees, enter the plot/point number only with the remainder of the fields blank. This entry is used in determining the number of sample plots/points. The number of sample plots/points is then used to determine the per acre average expansion factor. A plot/point number of 0 is not valid and will be rejected by ORGANON.

## 2. Species Code Number

A species code number is a 3-digit Forest Service code number to identify each tree species.

SWO-ORGANON accepts only the following tree species and corresponding species codes:

Species Code	Tree Species	Species Code	Tree Species
015	White Fir	351	Red Alder
017	Grand Fir	361	Pacific Madrone
081	Incense-cedar	431	Golden Chinkapin
117	Sugar Pine	492	Pacific Dogwood
122	Ponderosa Pine	631	Tanoak
202	Douglas-Fir	805	Canyon Live Oak
231	Pacific Yew	815	Oregon White Oak
242	Red Cedar	818	California Black Oak
263	Western Hemlock	920	Willow
312	Bigleaf Maple		

NWO-ORGANON and SMC-ORGANON accepts only the following tree species and corresponding species codes:

Species Code	Tree Species	Species Code	Tree Species
017	Grand Fir	351	Red Alder
202	Douglas Fir	361	Pacific Madrone
231	Pacific Yew	492	Pacific Dogwood
242	Red Cedar	815	Oregon White Oak
263	Western Hemlock	920	Willow
312	Bigleaf Maple		

RAP-ORGANON accepts only the following tree species and corresponding species codes:

Species Code	Tree Species	Species Code	Tree Species
202	Douglas Fir	351	Red Alder
242	Red Cedar	492	Pacific Dogwood
263	Western Hemlock	920	Willow
312	Bigleaf Maple		

For any tree species not listed, assign a code to the tree from the list above that closely resembles the growth of your unlisted tree species.

### **3. Diameter at Breast Height**

The diameter at breast height is the outside diameter measured in inches (to the nearest one-tenth inch) at the tree's breast height (approximately 4 1/2 feet above ground on uphill side) on all trees greater than breast height.

### **4. Total Tree Height**

The total tree height is the height of the tree from ground level to the crown's tip measured in feet (to the nearest one-tenth foot) for all trees.

### **5. Crown Ratio**

The crown ratio is the length in feet of the live crown (CL) divided by the total tree height (HT). Crown length is the total tree height minus the height to crown base (HTCB). In symbolic terms, crown ratio is computed by:

$$R = CL/HT \quad \text{or} \quad 1.0 - HTCB/HT$$

When determining the base of the live crown, ignore epicormic and short branches less than 3 feet long. For trees of uneven crown length in the SWO, NWO, and SMC version of ORGANON, visually transfer lower branches on the longer side to fill holes in the upper portion of the shorter side to generate a full, even crown. For the RAP version of ORGANON, crown base is defined as the last contiguous live whorl from the top of the tree in which  $\frac{3}{4}$  of the branches in the whorl are alive.

### **6. Expansion Factor**

The expansion factor is the weight (i.e., number of trees per acre) that each sample tree represents on each plot/point. The program automatically converts this to the stand average (ORGANON divides by the number of points). For a fixed area plot, the expansion factor is the reciprocal of the area of the plot in acres. For variable plots, the expansion factor is the basal area factor in square feet divided by the tree's basal area.

## 7. Radial Growth

The 5-year radial growth inside bark at breast height is measured in decimal inches determined from increment cores. If measured during a growing season, be sure to ignore the current year's growth.

## 8. User Code

A user code is a 1- or 2-digit number assigned to a tree. The user code allows you to designate the tree in some predetermined manner for thinning. For example, you might code all mistletoe infected trees with one code and assign another code to all non-crop trees. Managers can select these specially coded trees for removal or other action.

## C. ***Minimum Required Tree Measurements***

A stand is described by entering the characteristics of sample trees contained in that stand. You must enter certain measurements of each sample tree, while other measurements are not absolutely required. The minimum required measurements for each tree are:

- plot/point number
- species code number
- diameter outside bark at breast height
- expansion factor

If expansion factors are missing from the input file, ORGANON computes the expansion factors based on user-supplied information concerning the sampling design that measured the stand. The remaining optional variables provide more accurate diameter growth predictions and additional thinning capabilities.

## **D. Strongly Recommended Tree Measurements**

In addition to the required tree variables, you should also include the following measurements:

- total tree height
- crown ratio

If not included, they are predicted from equations representing regional averages. If these measurements are subsampled, the regional average equations are calibrated to the actual measurements for the stand. For more accurate results, you are strongly urged to collect as many measurements as possible.

## **E. Optional Tree Measurements**

The following set of tree variables is optional for input:

- prior 5-year radial growth
- user code

## **F. Tree Data File Creation**

Once the necessary measurements have been taken on the stand, the tree measurement data must be entered into a file for input into ORGANON. This can be done using a word processing program or it can be done within ORGANON itself.

### **1. Creating a Tree Data File with a Word Processor**

You can use any word processor that generates an ASCII file to create the data file. An ASCII file is a file that contains no formatting characters (word wrap, formatting, etc.). This is generally referred to as a flat, or non-document file. Wordstar, WordPerfect, MS-Word, MS-DOS Edit, and MS-Windows NotePad can create this type of file. Check your word processor manual for instructions on creating an ASCII file.

Use one line (all characters up to a carriage return) to

enter all the data for one tree. The total number of lines in the file should equal the total number of trees being entered plus the number of plots/points without trees.

All data elements should be right justified in their field. If an optional element is not included, enter blanks in its field. For plots or points without trees, be sure to enter the plot/point number only with the remainder of the fields blank. In the following description, an integer refers to a whole number (no decimal point, i.e., 365). A real number implies a decimal number (i.e., 27.4).

Follow the example in the table below to create a data file using a word processor.

<u>Element</u>	<u>Col #</u>	<u>Comment</u>
1	1-3	Plot/Point number (INTEGER). REQUIRED. (e.g., 10)
2	5-7	Species Code number (INTEGER). REQUIRED. One of the 3-digit codes from section SPECIES CODE NUMBER. (e.g., 202)
3	9-13	Diameter Outside Bark at Breast Height in inches (REAL-1 decimal place). REQUIRED. (e.g., 27.5)
4	15-19	Total Tree Height in feet (REAL-1 decimal place). STRONGLY RECOMMEND (5 blanks if omitted). (e.g., 134.9)
5	21-24	Crown Ratio (REAL-2 decimal places). STRONGLY RECOMMEND (4 blanks if omitted). (e.g., .63)
6	26-31	Expansion Factor for plot/point (REAL-2 decimal places). ORGANON will divide this value by the number of plot/points determined during data input. OPTIONAL (6 blanks if omitted). (e.g., 25.24)
7	33-37	Radial Growth inside bark in inches (REAL-2 decimal places). OPTIONAL (5 blanks if omitted). (e.g., 2.91)
8	39-40	User Code (INTEGER). Any designated identification number for user specified thinning. OPTIONAL (2 blanks if omitted). (e.g., 2)

SAMPLE TREE DATA INPUT LINE

Column	1	2	3	4
	1234567890123456789012345678901234567890			
	<b>10 202 27.5 134.9 .63 25.24 2.91 2</b>			
POINT	PLOT	\ DBH	HT CR EXP RADIAL GRO	USER CODE
	SPECIES			

SAMPLE TREE DATA INPUT LINE WITH MISSING ELEMENTS

Column	1	2	3	4
1234567890123456789012345678901234567890				
<b>10 202 27.5</b>	<b>.63</b>	<b>2.91</b>		
PLOT	\ DBH	HT	CR EXP	RADIAL L USER CODE
POINT	SPECIES			GRO

SAMPLE TREE DATA FILE  
WITH ERRORS AND OMISSIONS

COLUMNS			
1	2	3	4
1234567890123456789012345678901234567890			
1 202 7.8 43.3 .73			
1 202 45.9 .94			
1 202 9.0 40.2 .89			
1 202 11.1 .99			
1 202 4.9 35.6 .98			
1 202 3.3 21.9 .86			
1 202 3.0 19.8 .85			
2 202 10.4 45.0 .88			
2 202 9.8 46.6 .91			
2 202 11.6 58.3 .95			
2 202 4.1 31.2 .89			
2 202 7.6 43.6 .92			
2 202 4.4 30.4 .92			
2 202 4.6 35.3 .73			
2 202 .2 4.5 .87			
3 199 6.3 36.7 .92			
3 202 3.6 20.2 .95			
(blank line)			
3 202 3.9 22.5 .98			
4 202 5.1 30.7 .95			
5 (plot with no trees)			

## 2. Creating a Tree Data File in ORGANON

An optional method of creating an input data file exists within ORGANON. The ORGANON option prompts you to enter each of the tree data elements, one element at a time, one tree at a time. ORGANON formats the data in an ASCII file format. The ORGANON setup cannot be used to add a tree or modify a tree on an existing tree data file. However, you can use a word processor to add or edit an existing file. Another option is to use the on-line editor of ORGANON to add, delete or modify a tree record.

ORGANON TREE DATA FILE INPUT EXAMPLE

```
TREE # 1
Plot/Point Number (Required-Integer) ---> 1
Tree Species Code (Required-Integer) ---> 202
Diameter at Breast Height (Required-Real) ---> 7.8
Height in feet (Optional-Real) ---> 43.3
Crown Ratio (Optional-Real) ---> .73
Expansion Factor (Optional-Real) ---> <CR>
Radial Growth in inches (Optional-Real) ---> <CR>
User 2-digit thinning code (Optional-Integer) ---> 2
Species: 202
DBH: 7.8
HT: 43.3
CR: .73
EXP: .0
RADGRO: .00
USER: 2      Save this tree (Y) ? <CR>
Another tree (Y) ? <CR>
```

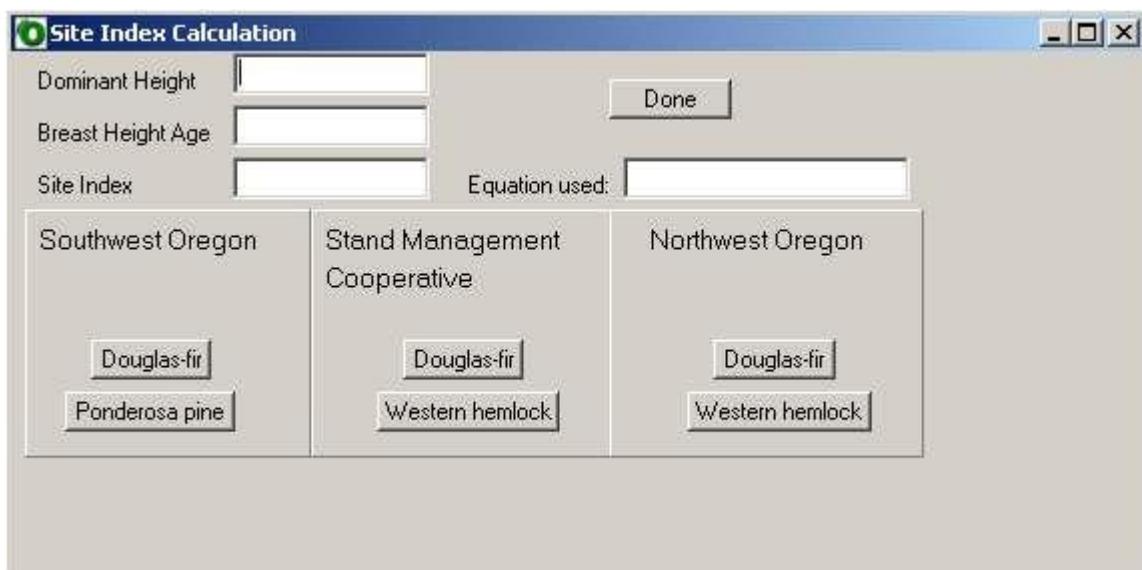
## IV. ORGANON Windows Interface

The ORGANON Windows Interface allows you to operate all of the components of ORGANON from a single windows based front-end. Through this interface you can start both the data editing and model execution components of ORGANON, utilize a built in site index calculator, run the plot yield calculation program, and get help about ORGANON.

These features are accessed via the menu bar at the top of the window. File->Close allows you to quit the windows interface. Clicking "Site Index" opens the site index calculator.

### A. Site Index Calculator

The Site Index Calculator is use to quickly determine appropriate site index values for use in ORGANON. After clicking the site index button, the calculator will appear in a new window.



To use the Calculator simply enter in the dominant height, the total height of trees in the dominant crown class, and the breast height age, the age of the trees after they have achieved 4.5 ft. in height. Valid values for these inputs depend on the version of the model you are running and the species for which you are calculating the site index. The following table summarizes the valid ranges for these values.

Version	SWO		SMC		NWO	
Species	Douglas-fir	Ponderosa Pine	Douglas-fir	Western Hemlock	Douglas-fir	Western Hemlock
Dominant Ht.	5-300	5-250	5-250	5-250	5-250	5-250
Breast Ht. Age	21-500	21-500	21-120	21-120	21-250	21-250

The site index calculator then uses these values to determine site index. The specific equations and how they are used to calculate site index depends upon the version of ORGANON to be run.

SWO-ORGANON uses the equations of Hann and Scrivani (1987) for Douglas-fir and ponderosa pine. These equations are applied to each of the breast height and total height measurements taken on a sample of at least six individual, site quality trees in the stand. The resulting tree site index values are then averaged to estimate the stand's site index.

NWO-ORGANON uses King's (1966) equation for Douglas-fir and Flewellings' unpublished equation for western hemlock. Both of these equations require that the top height (the average height of the 40-largest diameter, undamaged trees per acre) and the average breast height age of the top height trees be determined first and then entered into the equation to determine the stand's site index.

SMC-ORGANON uses Bruce's (1981) equation for Douglas-fir and Flewellings' unpublished equation for western hemlock. Both of these equations require that the top height (the average height of the 40-largest diameter, undamaged trees per acre) and the average breast height age of the top height trees be determined first and then entered into the equation to determine the stand's site index.

## ***B. Starting Organon Modules***

The ORGANON windows interface also allows the user to start both the Orgedit and Orgrun modules of ORGANON from within the same interface. Choosing Tools->Edit Input from the menu bar starts up the "Orgedit" ORGANON module which allows you to create input files for the ORGANON model either by reading raw data files or by entering in trees by hand. The features of this module are described in Section V "ORGANON Data Editing." Clicking on Tools->Run Model allows you to start the growth model portion of ORGANON. This component is described in Section VI "ORGANON Model Execution." Clicking on Tools->Run PLTYLD allows you to start the plot yield supplemental program. This component is described in Section IX "Supplemental Program PLTYLD." Both the modules and PLTYLD will appear in a new window that will close upon exit.

## V. ORGANON DATA EDITING

The first step in making an ORGANON run is to input the raw data, edit it for possible problems, and then prepare the final data file that will be used by the growth model itself. The raw input data file can have any name up to eight characters long. The resulting edited and prepared file will have the same name as the raw data file but with an extension of .INP added to it (after any existing extension is removed).

Upon execution, ORGANON first asks which version of the model is appropriate for the data set collected in the stand.

### ORGANON EXECUTION EXAMPLE

```
C:>CD\MODEL  
C:\MODEL>ORGANON
```

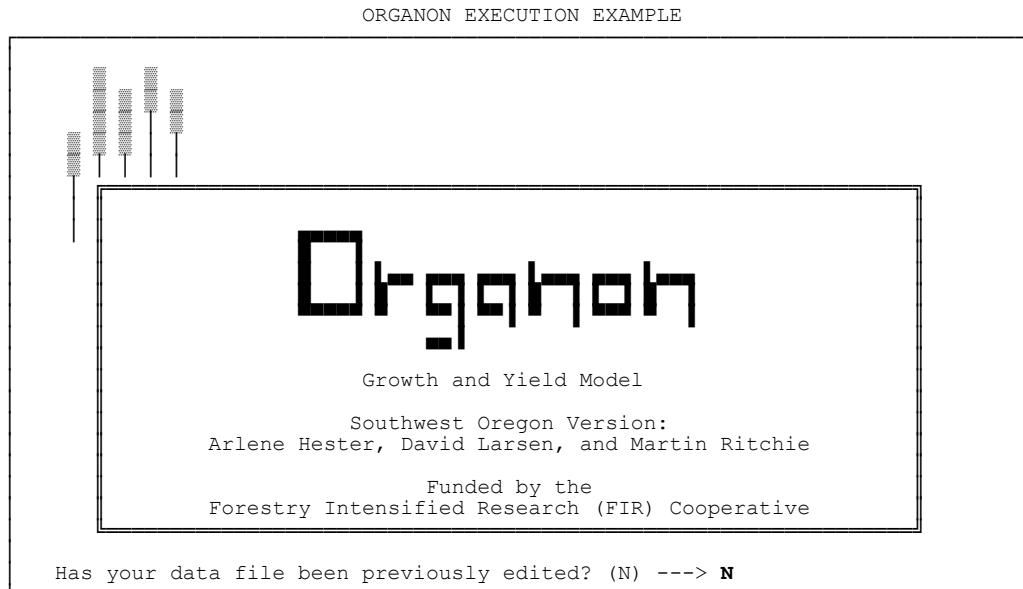
ORGANON  
ORegon Growth ANalysis and projection system  
by David W. Hann  
Oregon State University

Growth and Yield Model

Version 1: Southwest Oregon Mixed Conifer Forests  
Version 2: Northwest Oregon Forests  
Version 3: Stand Management Cooperative  
Version 4: Red Alder Plantation

Which version to run? (1=SWO, 2=WWV, 3=SMC, 4=RAP<CTRL-Q>=Quit) --->1

Files only have to be edited once by ORGANON. Therefore, ORGANON next asks whether the input data file has been previously edited in ORGANON (and a .INP file created). An answer of "yes" will start the growth model itself. An answer of "no" will start the data editing and preparation process. In the following example, the input data file has not been previously edited and, therefore, the answer is "N" for no.

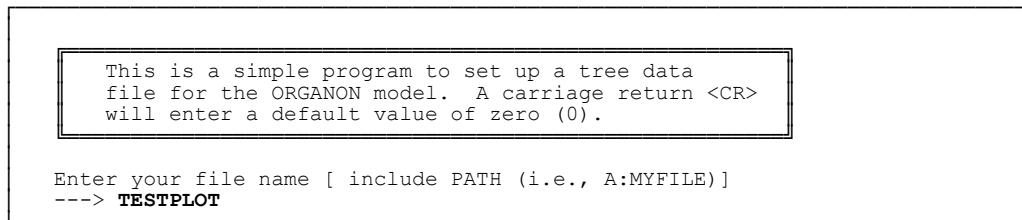
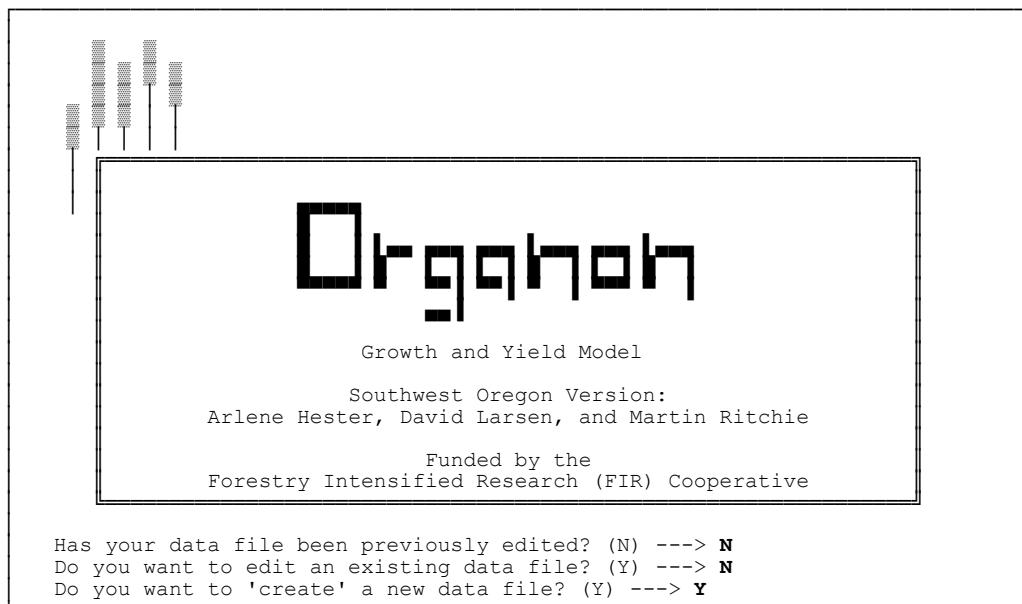


As explained in Section III.F (ORGANON INPUT DATA, Tree Data File Creation) of the Manual, the raw tree data measurements may be entered into a file using either a word processing program or the data entry option built into ORGANON. If the word processing option is used, then an "existing" file is available for editing. If the data entry option built into ORGANON is to be used, then a new file must be "created" before editing.

## A. Create a New Data File

In the following example, a new raw data file is to be created in ORGANON using the option describe in Section III.F.2 (ORGANON INPUT DATA, Tree Data File Creation, Creating a Tree Data File in ORGANON) of the Manual. The name of the file to be 'created' in ORGANON will be 'TESTPLOT' with no extension. Once 'TESTPLOT' has been created, then it must be edited as an "existing" file.

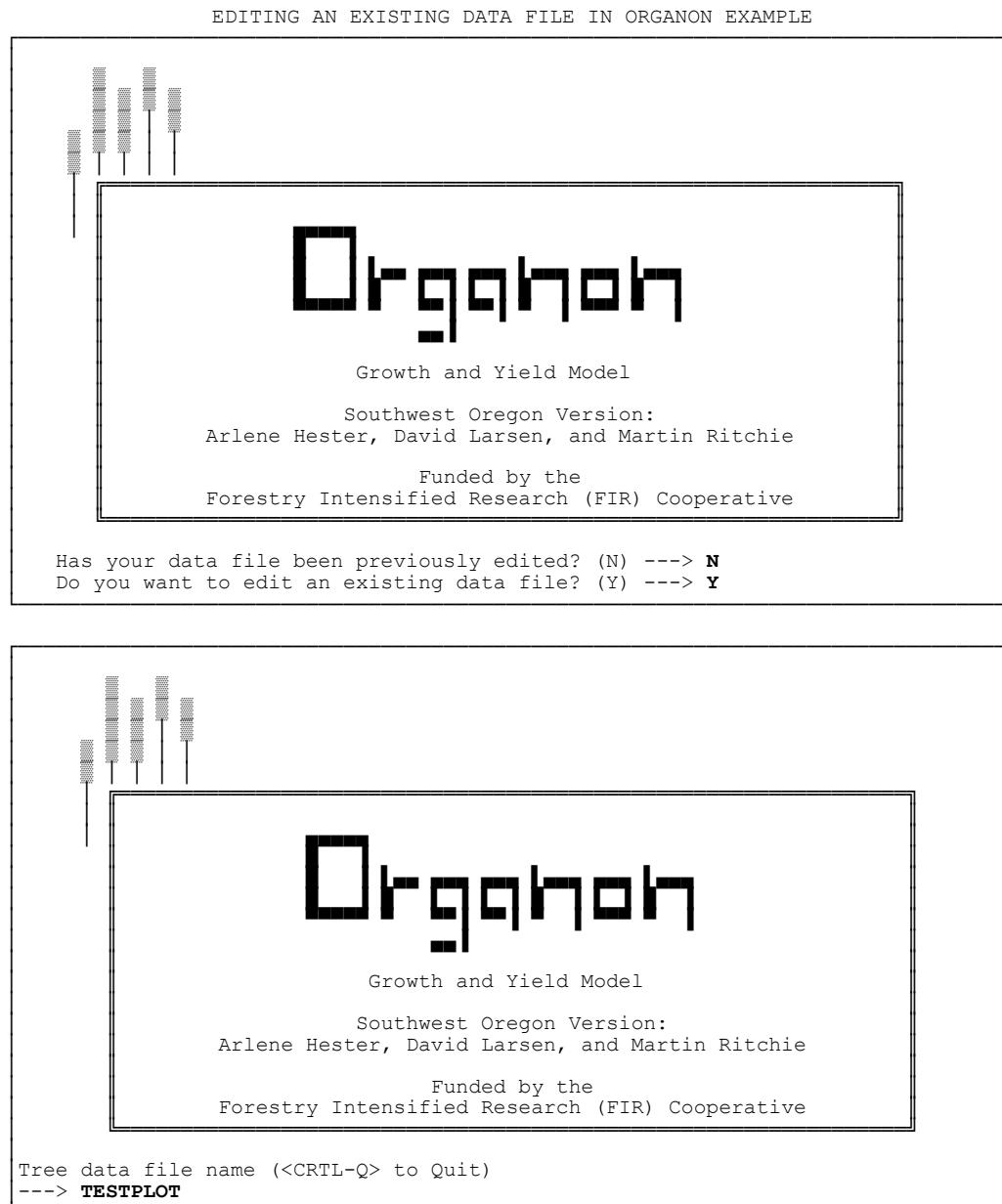
### CREATING A NEW DATA FILE IN ORGANON EXAMPLE



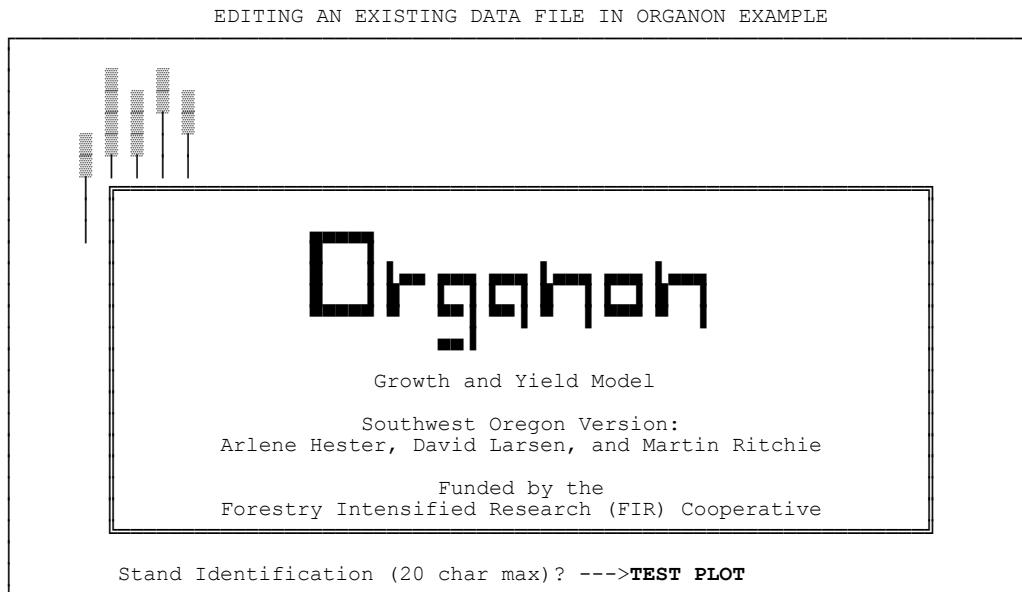
The individual tree data is then entered as shown in Section III.F.2 (ORGANON INPUT DATA, Tree Data File Creation, Creating a Tree Data File in ORGANON) of the Manual.

## **B. Editing an Existing Data File**

Once an existing data file has been created using either a word processing program or the entry option in ORGANON, the file's name must be entered into ORGANON.



Finally, a label of up to 20 characters in length must be entered to identify the stand. This label will be used on the tables, graphs and printer output files.



## C. **Data Read and Edit**

### 1. **Error and Warning Detection**

As ORGANON reads an input file, the raw data is scanned for errors. As errors are detected, only the trees with errors are identified and displayed on the screen unless you request the model to list every tree record in the file. If you request this option, ORGANON prompts you to connect and ready the printer. Ignore this prompt if a hard copy is unnecessary. The printer MUST be connected later in the program to print reports if they are sent to the printer. After all the data are read, ORGANON provides an error summary. These errors may include:

1. Plot/Point number of 0
2. Missing variables that are REQUIRED
3. DBH of 0 inches
4. Illegal species code
5. Blank records
6. Total tree height of 4.5 feet or under

Along with the fatal errors detected, ORGANON also

displays if STRONGLY RECOMMENDED and OPTIONAL variables have been entered and if any plots/points were entered with "no trees."

ERROR AND WARNING DETECTION

Display data as well as errors during read? (N) ---> <CR>

```
*** DBH=0.0 FOR TREE    2 IS NOT VALID
*** HEIGHT <= 4.5" FOR TREE   15 IS NOT VALID
*** ILLEGAL SPECIES CODE 199 FOR TREE   16
*** ILLEGAL PLOT/POINT NUMBER OR BLANK LINE FOR TREE   18
      *** RECORD WILL BE IGNORED***
*** WARNING -- POINT 5 HAS NO TREES
```

20 records have been read...
<CR> to continue...

The following are the data scan results...
Errors MUST be corrected before model is run.

```
ILLEGAL SPECIES CODES ARE PRESENT...
All point numbers are legal...
ILLEGAL DBH EXISTS ...
THERE ARE ILLEGAL TREE HEIGHTS...
All crown ratios are present...
THERE ARE EXPANSION FACTORS MISSING... (not reqd)
SOME RADIAL GROWTHS WERE NOT INPUT... (not reqd)
THERE ARE MISSING TREE HEIGHTS... (not reqd)
1 PLOT WITH NO TREES
```

Data entry is completed...
You will be entering the correction module
<CR> to continue...

## 2. Error Correction

After the tree data has been read and an error and warning listed, you can use a simple on-line editor to add, delete, list or change any of the tree record variables. You can inspect a list of all errors to be corrected if desired. Entering a carriage return (<CR>) terminates the on-line editor as long as all detected errors have been corrected.

ERROR CORRECTION EXAMPLE	
<b>ORGANON ON-LINE EDITOR OPTION</b>	
<pre>20 RECORDS CURRENTLY IN FILE TESTPLOT CONSISTING OF: 19 original tree records  1 original plot with no trees  0 added tree records  0 added plots with no trees  0 records flagged for deletion  0 tree records  0 plot records with no trees 20 records remaining after deletion  19 tree records  1 plot record with no trees</pre>	
ENTER	TO PERFORM
ERR LST ADD (record number)	ERRORS to correct LIST all records ADD a record EDIT (record number) <CR> to END ]
CORRECT --->	

## a. Errors to Correct

You must correct all fatal errors before the model can operate. When ORGANON reads data, errors are tagged for later detection. Entering 'ERR' during an on-line editing session lists all remaining record errors to correct.

ERROR CORRECTION EXAMPLE	
<b>ORGANON ON-LINE EDITOR OPTION</b>	
<hr/> 20 RECORDS CURRENTLY IN FILE TESTPLOT CONSISTING OF: 19 original tree records 1 original plot with no trees 0 added tree records 0 added plots with no trees 0 records flagged for deletion 0 tree records 0 plot records with no trees 20 records remaining after deletion 19 tree records 1 plot record with no trees <hr/>	
ENTER	TO PERFORM
ERR LST ADD (record number)	ERRORS to correct LIST all records ADD a record EDIT (record number) [ <CR> to END ]

CORRECT ---> **ERR**

Tree # 2 DBH = 0 Tree # 15 illegal tree height Tree # 16 bad species code  <CR> to continue...
---

## b. List All Records

You can, at any time, get a current listing of all tree records in the stand by using the LST option. This listing displays plots with no trees, as well as all the records flagged for deletion. Records flagged for deletion display '\*\*\*' for a species code.

ERROR CORRECTION EXAMPLE																
ORGANON ON-LINE EDITOR OPTION																
20 RECORDS CURRENTLY IN FILE TESTPLOT CONSISTING OF: 19 original tree records 1 original plot with no trees 0 added tree records 0 added plots with no trees 0 records flagged for deletion 0 tree records 0 plot records with no trees 20 records remaining after deletion 19 tree records 1 plot record with no trees																
ENTER TO PERFORM																
ERR	ERRORS to correct															
LST	LIST all records															
ADD	ADD a record															
(record number)	EDIT (record number)															
[ <CR> to END ]																
CORRECT ---> <b>LST</b>																
CROWN EXP USER																
TREE	POINT	SPECIES	DBH	HEIGHT	RATIO	FACTOR	RADGRO	CODE								
1	1	DF	7.8	43.3	.73	.00	.00	0								
2	1	DF	.0	45.9	.94	.00	.00	0								
3	1	DF	9.0	40.2	.89	.00	.00	0								
4	1	DF	11.1	.0	.99	.00	.00	0								
5	1	DF	4.9	35.6	.98	.00	.00	0								
6	1	DF	3.3	21.9	.86	.00	.00	0								
7	1	DF	3.0	19.8	.85	.00	.00	0								
8	2	DF	10.4	45.0	.88	.00	.00	0								
9	2	DF	9.8	46.6	.91	.00	.00	0								
10	2	DF	11.6	58.3	.95	.00	.00	0								
11	2	DF	4.1	31.2	.89	.00	.00	0								
12	2	DF	7.6	43.6	.92	.00	.00	0								
13	2	DF	4.4	30.4	.92	.00	.00	0								
14	2	DF	4.6	35.3	.73	.00	.00	0								
15	2	DF	.2	4.5	.87	.00	.00	0								
16	3	**	6.3	36.7	.92	.00	.00	0								
17	3	DF	3.6	20.2	.95	.00	.00	0								
18	3	DF	3.9	22.5	.98	.00	.00	0								
19	4	DF	5.1	30.7	.95	.00	.00	0								
20	5	PLOT WITH NO TREES														
<CR> to continue...																

### c. Modify a Record

To modify any variable of a tree, or to delete a tree entirely, first enter the tree record number. This tree number is the record number assigned during data file input. You can also obtain this number by selecting the LST option above and listing the file on the screen. This number is useful only for editing purposes.

After you select a record number, ORGANON displays all variables of that record. All modifications to tree variables made during on-line editing are saved only in the '.INP' file. The original raw data file remains unchanged. Strongly Recommended and Optional tree variables that were not entered appear as 0 during on-line editing. These zero values do not need to be corrected as the DATA COMPLETION routine calculates and fills in the missing values. Errors in the Strongly Recommended and Optional variables, however, must be corrected as these values are used to calculate calibration factors in the DATA COMPLETION routine.

Select a variable for modification by entering the variable's number (a value from 1 to 8). ORGANON prompts you for the new value for that variable. All data checks made during initial data input are repeated as each new variable value is entered. After the new value for a tree record is accepted, all tree variables are again displayed, as are any changes made.

If an entire tree record is to be deleted, select its tree number when prompted. After all the tree variables are displayed, select option 9--DELETE/UNDELETE RECORD. The tree remains in the list, but is flagged for deletion after you leave the editor. You can also delete a plot with no trees in this manner. Option 9 is also useful to remove the deletion flag in order to restore a tree to the tree list.

ERROR CORRECTION EXAMPLE

ORGANON ON-LINE EDITOR OPTION	
20 RECORDS CURRENTLY IN FILE TESTPLOT CONSISTING OF: 19 original tree records 1 original plot with no trees 0 added tree records 0 added plots with no trees 0 records flagged for deletion 0 tree records 0 plot records with no trees 20 records remaining after deletion 19 tree records 1 plot record with no trees	
ENTER	TO PERFORM
ERR LST ADD (record number)	ERRORS to correct LIST all records ADD a record EDIT (record number) [ <CR> to END ]
CORRECT ---> <b>2</b>	

Enter variable # of tree: 2
1) POINT: 1 2) SPECIES: 'DF' 3) DIAMETER: .0 4) HEIGHT: 45.9 5) CROWN RATIO: .94 6) EXPANSION: .00 7) RADIAL GROWTH: .00 8) USER CODE: 0 9) ** DELETE/UNDELETE ** [ <CR> to END ]
ITEM # TO CORRECT ---> <b>3</b>
Enter variable value for item 3) <b>11.1</b>

Enter variable # of tree: 2
1) POINT: 1 2) SPECIES: 'DF' 3) DIAMETER: 11.1 4) HEIGHT: 45.9 5) CROWN RATIO: .94 6) EXPANSION: .00 7) RADIAL GROWTH: .00 8) USER CODE: 0 9) ** DELETE/UNDELETE ** [ <CR> to END ]
ITEM # TO CORRECT ---> <b>&lt;CR&gt;</b>

ORGANON ON-LINE EDITOR OPTION	
20 RECORDS CURRENTLY IN FILE	
TESTPLOT	
CONSISTING OF:	
19 original tree records	
1 original plot with no trees	
0 added tree records	
0 added plots with no trees	
0 records flagged for deletion	
0 tree records	
0 plot records with no trees	
20 records remaining after deletion	
19 tree records	
1 plot record with no trees	
ENTER	TO PERFORM
ERR	ERRORS to correct
LST	LIST all records
ADD	ADD a record
(record number)	EDIT (record number)
[ <CR> to END ]	

CORRECT ---> **20**

Enter variable # of tree: 20
1) POINT: 5
2) SPECIES: '
3) DIAMETER: .0
4) HEIGHT: .0
5) CROWN RATIO: .00
6) EXPANSION: .00
7) RADIAL GROWTH: .00
8) USER CODE: 0
9) ** DELETE/UNDELETE **
[ <CR> to END ]

ITEM # TO CORRECT ---> **9**

Record # 20 flagged for deletion...

<CR> to continue...

## d. Add a Record

The ADD option allows you to add new records to the tree list. A 'null' record is displayed on the screen and each variable of the record is subsequently modified to describe the tree added. You can add a plot with no trees to the tree list by specifying ADD, designating a plot number, and leaving the remaining variables zero.

### ERROR CORRECTION EXAMPLE

ORGANON ON-LINE EDITOR OPTION	
ENTER	TO PERFORM
ERR LST ADD (record number)	ERRORS to correct LIST all records ADD a record EDIT (record number) [ <CR> to END ]

Enter variable # of tree: 21
1) POINT: 0 2) SPECIES: ' ' 3) DIAMETER: .0 4) HEIGHT: .0 5) CROWN RATIO: .00 6) EXPANSION: .00 7) RADIAL GROWTH: .00 8) USER CODE: 0 9) ** DELETE/UNDELETE ** [ <CR> to END ]
ITEM # TO CORRECT ---> 1
Enter variable value for item 1) 8
(continue entering variables for new tree)

ERROR CORRECTION EXAMPLE cont.

```
ORGANON ON-LINE EDITOR OPTION
21 RECORDS CURRENTLY IN FILE 'TESTPLOT'
TESTPLOT
CONSISTING OF:
 19 original tree records
   1 original plot with no trees
   1 added tree record
   0 added plots with no trees
  2 records flagged for deletion
   1 tree record
   1 plot record with no trees
19 records remaining after deletion
 19 tree records
   0 plot records with no trees
[ <CR> to end ]
CORRECT ---> 15
```

NOTE: To continue to follow the examples shown in this manual using test file TESTPLOT, perform the following corrections.

Record #15 - change height to 5.2'  
Record #16 - make species code 202 (DF)  
Record #21 - delete added point 8 record

```
CORRECT ---> <CR>
```

```
4 points determined for TESTPLOT
```

## **D. Productivity Variables**

### **1. Site Indexes**

SWO-ORGANON requests two site indexes--Douglas-fir and Ponderosa Pine. You must enter at least one of the two site indexes. If both values are entered, both are used. If only one value is entered, the site index not entered is calculated from the entered site index.

```
Douglas Fir (total height) site index? ---> 109.4
Ponderosa Pine (total height) site index? ---> 102.9
```

NWO-ORGANON requests two site indexes--Douglas-fir and western hemlock.

SMC-ORGANON requests two site indexes--Douglas-fir and western hemlock.

RAP-ORGANON requests two site indexes--Red Alder and Douglas-fir.

Guidelines for measuring and a site index calculator can be found in section IV.A. Site Index Calculator.

### **2. Even/Uneven Age Stands**

You may enter the sample stand as an even- or uneven-aged stand.

```
Even-age Stand? (Y) ---> <CR>
```

### 3. Stand Age

If you enter an even-age stand, ORGANON prompts you for the stand age as measured by breast height diameter. You have the option to enter the number of years to breast height to determine total stand age. If this entry is blank, ORGANON determines the total stand age.

Total stand age will be the age displayed in all tables and plots, and in calculations of mean annual increment (MAI). The growth and mortality equations in ORGANON do not utilize stand age as an independent variable.

```
Even-age Stand? (Y) ---> <CR>
Breast height stand age? ---> 28

Do you want to enter number of years to reach breast height?
(N - ORGANON will calculate) ---> <CR>
```

## E. Data Completion

### 1. Expansion Factor

ORGANON allows very flexible calculation of expansion factors from a wide variety of sample systems.

Three methods for defining an expansion factor are available:

- describe expansion factors
- use default expansion factor file
- create default expansion factor file

#### EXPANSION FACTOR INPUT METHOD EXAMPLE

```
[EXPANSION DEFAULT SELECTION ]
1 - Describe Expansion
2 - Use Default Expansion file 'ORGANON.EXP'
3 - Create 'ORGANON.EXP'
[ <CR> = Describe Expansion ]
INPUT --->
```

## a. Describe Expansion Factors

With this input method, ORGANON prompts you to describe the sample unit. A sample unit is composed of one or more sub-sample units at a single location and with a common center. These subsamples are called "nested subsamples." ORGANON allows a maximum of five nested subsamples per sample unit.

You can label fixed area subsample values by the square foot size, by the fractional amount of an acre, or by the radius of a circular plot.

You can label a variable radius plot/point subsample by its basal area factor.

When you select nested subsamples, the diameter of each tree determines the subsample into which it lies and the appropriate expansion factor formula for that subsample. To set these diameter limits for nested subplots, ORGANON prompts you to list the lower diameter limit for each subplot.

### DESCRIBE EXPANSION FACTOR EXAMPLE

```
INPUT ---> 1
Did you use nested subsamples? ---> Y
Enter the number of subsamples ---> 3
```

```
START WITH SMALLEST DIAMETER SUBSAMPLE
SUBSAMPLE 1:
Fixed radius/area (ie. sq ft)-- F
Variable radius (ie. point)---- V
(enter F or V) ---> F
Fixed area plot determined by...
1. Square Feet
2. Fractional Acres (X as in 1/X)
3. Radius (in feet)
ENTER 1, 2 OR 3 ---> 3
Enter value ---> 7.78
```

```
SUBSAMPLE 2:
Fixed radius/area (ie. sq ft)-- F
Variable radius (ie. point)---- V
(enter F or V) ---> F
Fixed area plot determined by...
1. Square Feet
2. Fractional Acres (X as in 1/X)
3. Radius (in feet)
ENTER 1, 2 OR 3 ---> 3
Enter value ---> 15.56
```

DESCRIBE EXPANSION FACTOR EXAMPLE (continued)

SUBSAMPLE 3:

Fixed radius/area (ie. sq ft)-- F  
Variable radius (ie. point)---- V  
(enter F or V) ---> **V**  
Enter basal area factor in sq. ft. (BAF) ---> **20**

EXPANSION FACTORS FOR FILE: TESTPLOT  
SUBSAMPLE 1:  
    Fixed -- PLOT RADIUS (FT) =      7.78  
SUBSAMPLE 2:  
    Fixed -- PLOT RADIUS (FT) =      15.56  
SUBSAMPLE 3:  
    Variable radius - 20.0 BAF  
  
Would you like to re-enter? (N) ---> **<CR>**

Upper and lower limits must be assigned to the 3 subsamples.  
Enter limits and adjustment will be made as follows:

0 4 8 12 (4 subsamples) results in:  
1) 0.0 < DBH <= 4.0"      (SUBSAMPLE 1)  
2) 4.0 < DBH <= 8.0"      (SUBSAMPLE 2)  
3) 8.0 < DBH <= 12.0"      (SUBSAMPLE 3)  
4) DBH > 12.0"      (SUBSAMPLE 4)

Enter limits for subsamples ---> **0 4 8**

LIMITS HAVE BEEN SET AS FOLLOWS:

1) .0 < DBH <= 4.0"      (SUBSAMPLE 1)  
2) 4.0 < DBH <= 8.0"      (SUBSAMPLE 2)  
3) DBH > 8.0"      (SUBSAMPLE 3)

Would you like to re-enter? (N) ---> **<CR>**

\*\*\* please wait - determining height calibration value

## b. Use Default Expansion Factor File

A default expansion file, ORGANON.EXP, which describes a commonly used sampling method, can provide answers to all of ORGANON's prompts as described in input method 1.

When you select the default expansion file as the input method, ORGANON displays the file and prompts you to verify acceptance of the sampling description. If the default description is unacceptable, you must select another sampling input method.

```
USE DEFAULT EXPANSION FILE EXAMPLE

[ EXPANSION DEFAULT SELECTION ]
1 - Describe Expansion
2 - Use Default Expansion file 'ORGANON.EXP'
3 - Create 'ORGANON.EXP'
[ <CR> = Describe Expansion ]

INPUT ---> 2

EXPANSION FACTORS FOR FILE: TESTPLOT

SUBSAMPLE 1:
    Fixed -- PLOT RADIUS (FT) =      7.78
SUBSAMPLE 2:
    Fixed -- PLOT RADIUS (FT) =     15.56
SUBSAMPLE 3:
    Variable radius - 20.0 BAF

LIMITS HAVE BEEN SET AS FOLLOWS:
    1)   .0 < DBH <=  4.0"    (SUBSAMPLE 1)
    2)  4.0 < DBH <=  8.0"    (SUBSAMPLE 2)
    3)  DBH >   8.0          (SUBSAMPLE 3)

Reject these defaults? (N) ---> <CR>
```

## c. Create Default Expansion Factor File

In order to avoid repetition when a sampling unit description is used frequently, ORGANON can create a default file containing that description. The file is created responding to prompts as previously described in input method 1. Thereafter, the default file can be used to "answer" prompts by selecting input method 2.

## 2. Height and Height Calibration

ORGANON makes two passes through the input data file to determine height calibration values and to generate missing heights. The first pass through the data predicts heights for all trees in the stand having measured heights. ORGANON uses this predicted height along with the measured height to determine a calibration value by species, using weighted, simple linear regression through the origin. If the calibration value for a species is not significantly different ( $p=0.99$ ) from 1.0, the calibration value is set to 1.0. If the calibration value is determined to be greater than 2.0 or less than 0.5, the calibration value for that species is set to 2.0 or 0.5 respectively. A calibration value of 1.4 (or .85) signifies that the sample heights were on the average 1.4 times (or .85 times) the height determined by the height/diameter equations developed for ORGANON. These calibration values are used during prediction of missing heights for all species and during height growth for minor species. You can specify the use of these values during growth before each ORGANON run (see RUN DEFAULTS).

### HEIGHT AND HEIGHT CALIBRATION EXAMPLE

```
*** please wait - determining height calibration value
DOUGLAS FIR ht generation calibration value      =   .70   ( 18)
*** please wait --- missing heights are being calculated
      1 tree height predicted from 18 entered heights
<CR> to continue
```

HT's  
entered

### 3. Crown Ratio and Crown Ratio Calibration

ORGANON makes two passes through the input data file to determine crown ratio calibration and to generate missing crown ratios. The first pass through the data calculates crown ratios for all trees in the stand having measured crown ratios. ORGANON uses this predicted crown ratio along with the measured crown ratio to determine a calibration value by species, using weighted, simple linear regression through the origin. If the value for a species is not significantly different ( $p=0.99$ ) from 1.0, the calibration value is set to 1.0. If the calibration value is determined to be greater than 2.0 or less than 0.5, the calibration value for that species is set to 2.0 or 0.5, respectively. A calibration value of 1.4 (or .85) signified that the sample crown ratios were on the average 1.4 times (or .85 times) the crown ratios determined by the height-to-crown base equations developed for ORGANON. ORGANON uses this value to predict the missing crown ratios. During missing crown ratio calculations, height-to-crown base is calculated. If it is greater than 95% of the height, the height-to-crown base is set to 95% of the height. If the calibrated height-to-crown base is less than 0, the calibrated height-to-crown base is set to 0. During crown change, if the crown ratio is less than 0.5%, it is set to 0.5%. The use of these values during growth can be specified before each ORGANON run (see RUN DEFAULTS).

#### CROWN RATIO CALIBRATION EXAMPLE

```
*** please wait - determining crown ratio calibration value
      CR's
      entered
      I
DOUGLAS FIR crown ratio calibration value = 1.23  ( 19)
*** please wait - missing crown ratios are being calculated
0 crown ratios predicted from 19 entered crown ratios
<CR> to continue
```

#### 4. Diameter Growth and Diameter Growth Calibration

If you enter radial growth values, the diameter calibration values are determined by species using weighted, simple linear regression through the origin. The stand is back-dated and then grown in order to compare actual diameter growth with predicted diameter growth. No missing radial growths are predicted. If the calibration value for a species is not significantly different ( $p=0.99$ ) from 1.0, the calibration value is set to 1.0. If the calibration value is determined to be greater than 2.0 or less than 0.5, the calibration value for that species is set to 2.0 or 0.5, respectively. A calibration value of 1.4 (or .85) signifies that the radial growths were on the average 1.4 times (or .85 times) the radial growths determined by the equations developed for ORGANON. You can specify the use of these values to adjust diameter growth predictions before each ORGANON run (see RUN DEFAULTS).

DIAMETER CALIBRATION EXAMPLE

\*\*\* please wait - determining diameter calibration value

RADGRO's  
entered

1  
1

DOUGLAS FIR diameter growth calibration value = 1.00 ( 0 )

<CR> to continue

#### 5. Calibration and Actual Data Plots

After height, height-to-crown base, and diameter calibrations are made, plots are available for the calibrated variables listed above. These plots show predicted minus actual values (i.e., residuals) on the Y-axis, and predicted values on the X-axis for height, height-to-crown base and diameter growth. These plots are available both with and without the calibration ratios incorporated in the prediction. In addition, plots are also available showing actual height or crown ratio on the Y-axis and actual diameter on the X-axis. The plots that are available depend on the data entered (i.e., no plots with calibration are available if the calibration value is equal to 1.0). Output for these plots only goes to the screen. For hard copy output, use the appropriate DOS command. You may request these plots any number of times with different species. The digit actually plotted represents the number of input trees that fall into the range represented by that cell. The plots of calibrated and uncalibrated residuals over predicted values can be used to:

1. Examine the data for possible "outliers" (large positive or negative residuals) arising from measurement errors in the original input data. If "outliers" are to be corrected, you can use an external editor or the ORGANON editor by re-entering the data file.

2. Determine the effectiveness of the calibration value in improving the fit of the original input data to the regional equations in ORGANON. Ideally, the variation of the residuals across the predicted value should be homogeneous (the upper and lower bounds of the residuals should be horizontal), the sum of the residuals should be zero, and the residuals should exhibit no trends across the predicted values. If the calibrated residuals exhibit these features, then use of the calibration values is recommended. In the following example, the calibration value provided a better fit to the data. You should use the calibration value because, in this case, it gives a better fit to the data.

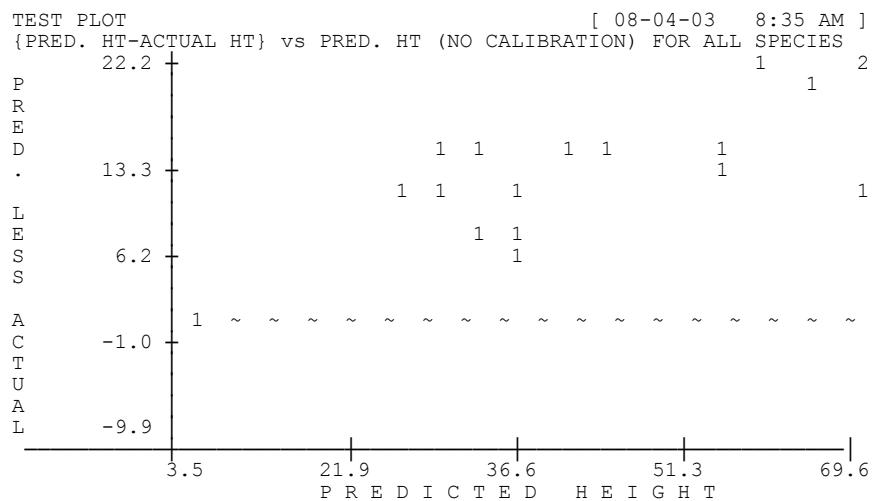
CALIBRATION AND ACTUAL PLOTS EXAMPLE

[ PLOTS OF CALIBRATION AND ACTUAL DATA ]  
[ No Calibration ]  
HT - (Predicted Height-Actual Height) vs Predicted Height  
CR - (Predicted CR-Actual CR) vs Predicted CR  
DG - (Predicted DG-Actual DG) vs Predicted DG  
[ With Calibration ]  
HTC - (Predicted Height-Actual Height) vs Predicted Height  
CRC - (Predicted CR-Actual CR) vs Predicted CR  
DGC - (Predicted DG-Actual DG) vs Predicted DG  
[ PLOTS OF ACTUAL DATA ]  
HTD - Actual Height vs Actual Diameter  
CRD - Actual Crown Ratio vs Actual Diameter  
DGD - Actual Diameter Growth vs Actual Diameter  
[ <CR> to End ]  
CALIBRATION PLOTS ---> HT

SPECIES GROUP (AL) ---> <CR> (See section SPECIES under (see section SPECIES under TABLE AND PLOT PARAMETERS for further explanation)

NOTE: The actual menu for test TESTPLOT would not include the DG, DGC and DGD because TESTPLOT had no radial growth measurements entered.

## CALIBRATION AND ACTUAL PLOTS EXAMPLE (continued)



<CR> to continue <CR>

[ PLOTS OF CALIBRATION AND ACTUAL DATA ]  
[ No Calibration ]

HT - (Predicted Height-Actual Height) vs Predicted Height  
CB - (Predicted-Actual) vs Predicted  
DG - (Predicted DG-Actual DG) vs Pred. DG  
[ With Calibration ]

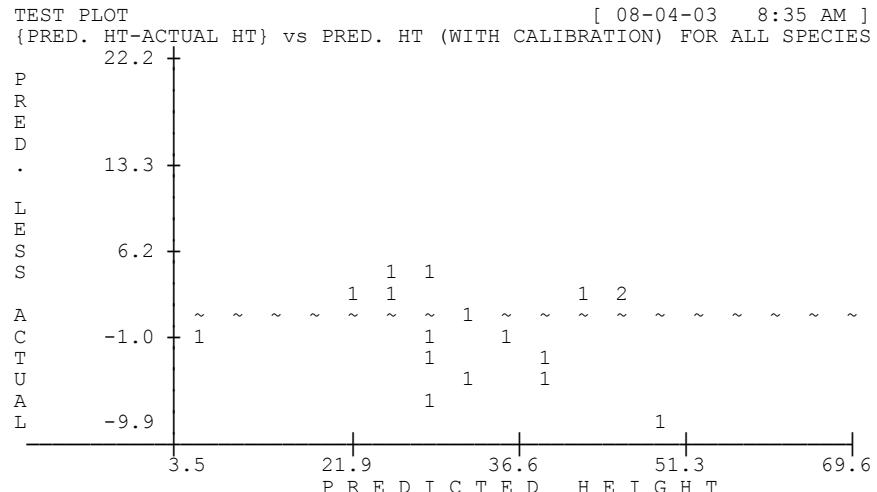
HTC - (Predicted Height-Actual Height) vs Predicted Height  
CBC - (Predicted-Actual) vs Predicted  
DGC - (Predicted DG-Actual DG) vs Pred. DG  
[ PLOTS OF ACTUAL DATA ]

HTD - Actual Height vs Actual Diameter  
CRD - Actual Crown Ratio vs Actual Diameter  
DGD - Actual Diameter Growth vs Actual Diameter  
[ <CR> to End ]

CALIBRATION PLOTS ---> **HTC**

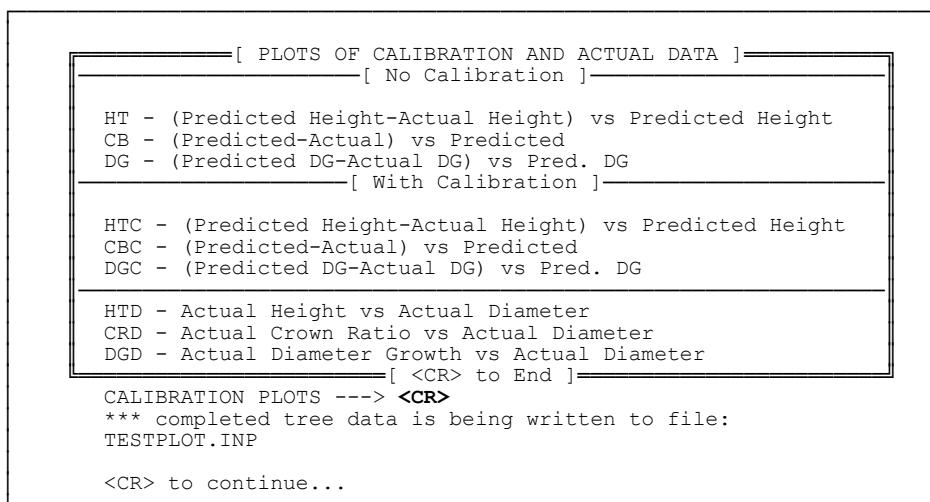
SPECIES GROUP (AL) ---> <CR>

CALIBRATION AND ACTUAL PLOTS EXAMPLE (continued)



After all requested plots are displayed, press the carriage return to erase the plot menu display. ORGANON writes the corrected, completed data file to an '.INP' file (see '.INP' FILES).

CALIBRATION AND ACTUAL PLOTS EXAMPLE (continued)



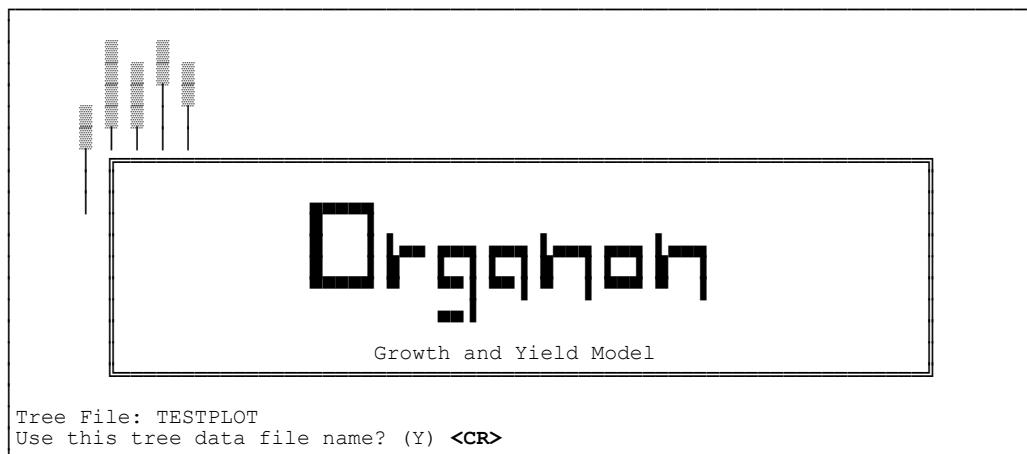
## ***F. '.INP' Files***

After ORGANON reads the raw data file, makes data corrections, and computes data completion and productivity values, the completed stand description file is saved and written to the same drive from which ORGANON read the original raw data file. The data file name is the original data file name (the root file name), with a 3-letter suffix or file name extension of '.INP'.

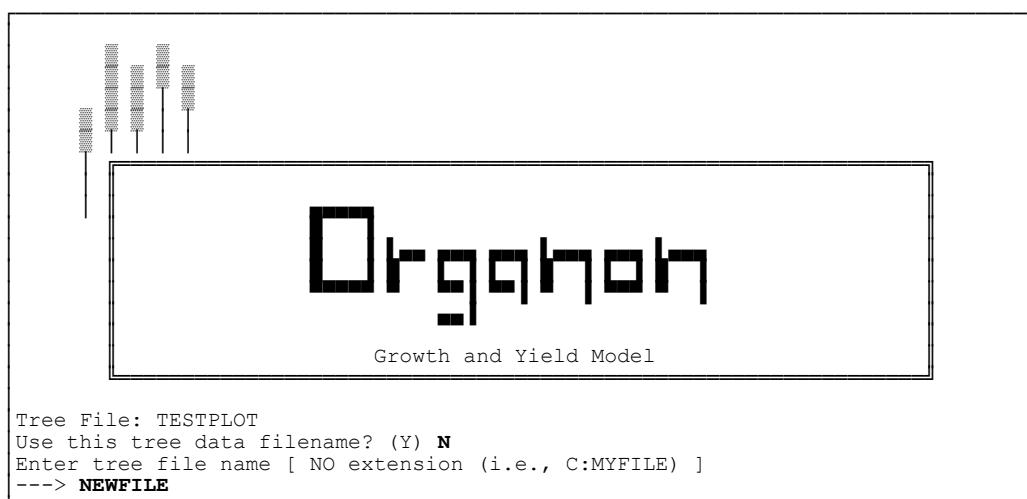
## VI. ORGANON MODEL EXECUTION

The main ORGANON growth module loads into memory after you have designated that raw data file(s) have been correctly processed and a valid '.INP' file exists for each raw data file. When the main ORGANON module has loaded, you must select which '.INP' data files you will enter and allow to be processed by the growth model. You must also choose a file to write the requested tables and plots to.

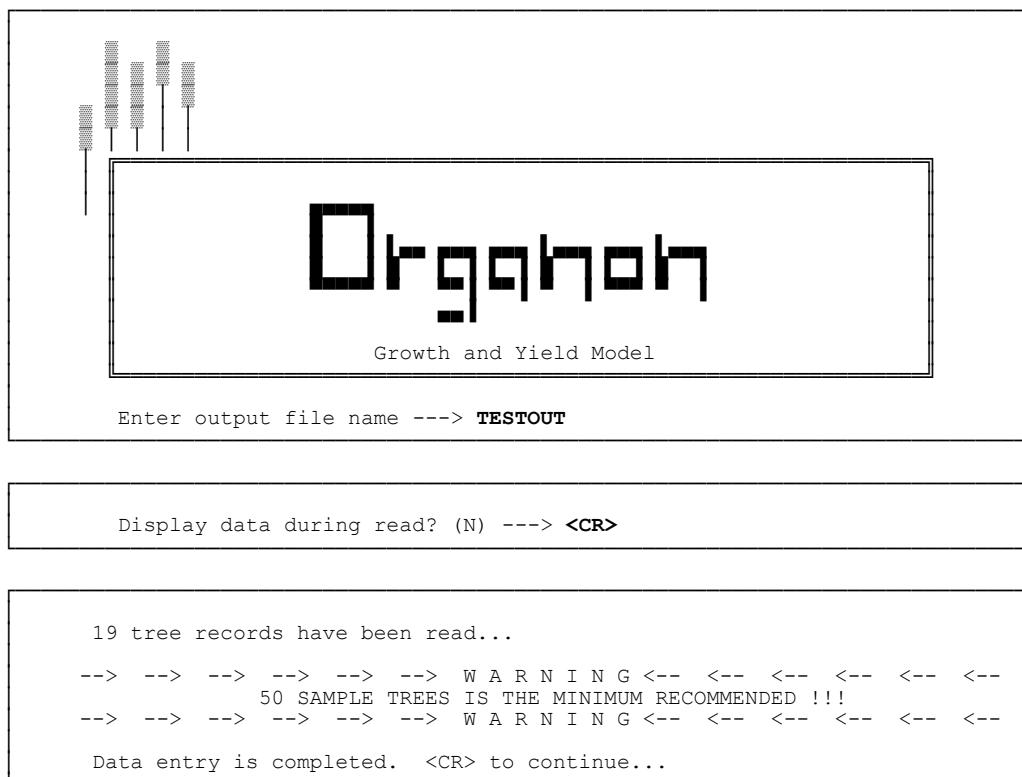
ORGANON saves the name of the file most recently opened by either the editing or execution modules. When the execution module is run it offers this filename as the default tree file. You may either accept this file name by typing either Y or Enter, or reject this filename by typing N and enter a new name. The following is an example of accepting the default filename.



The following is an example of rejecting the default filename and entering in a new filename called "NEWFILE".



After specifying the .INP filename, the user next needs to specify a filename for the output from the ORGANON run. The following is an example of specifying the output filename as "TESTOUT".



## A. *ORGANON Program Defaults and Specifications*

Twenty program variables form a parameter list that affects how ORGANON runs. ORGANON has a default value for each of these variables which can be used any time ORGANON runs (1 - System Defaults). You also have the option of defining and saving your own set of defaults for these variables (3 - Create 'ORGANON.DEF'). You can assign these values once and use them on any future ORGANON runs (2 - Use Default file 'ORGANON.DEF'). You may select the system defaults at any time. When prompted, select either the system defaults, your own previously defined defaults, or create your own new defaults. To create your own defaults, ORGANON starts with the set of system defaults and you modify these as desired. At the start of each program run, you may modify either system or user parameters. The parameter set selected remains active for only one ORGANON run.

```
[ DEFAULT INPUT SELECTION ]  
1 - Use System Defaults  
2 - Use Default file 'ORGANON.DEF'  
3 - Create 'ORGANON.DEF'  
[ <CR> = Use System Defaults ]  
INPUT ---> 1
```

A listing of ORGANON parameters and defaults follows.

## 1. Run Defaults

### a. Tripling (TRIPLING)

Tripling is designed to increase the sample size of the tree data set during a growth cycle. Tripling will continue during each growth cycle until the number of sample trees reaches either the maximum of 2000 or a number below the maximum for which another round of tripling would cause the resulting number of trees to exceed the maximum. Use of tripling causes more realistic projections of stand development through the use of stochastic elements added to the predictions. ORGANON execution time does increase somewhat due to the added time needed to process each of the additional sample trees. The default for this parameter is 'NO' (tripling will not occur).

## **b. Menu Display (DISPLAY MENUS)**

To assist you when running ORGANON, the model provides user friendly menus. After several runs, these menus may no longer be necessary and may slow more experienced users. You can eliminate these menu displays by selecting 'NO' on the menu display. Even with the menus off, a brief prompt (i.e., MANAGE-->) displays to indicate the type of input requested. If you are still uncertain about input choices, enter 'HELP' or '?' -- ORGANON will display the full menu. Execution time is slightly quicker when full menus are not displayed on the screen. The default for this parameter is 'YES' (display menus) .

## **c. Height Calibration (USE HEIGHT CALIB)**

When a data file is initially entered into ORGANON, height calibrations are calculated for each species. If you choose 'YES', the height calibration ratios modify the equations for use in growth predictions for hardwoods and Western Hemlock. If the calibrations were determined from actual tree measurement inputs, the growth models are calibrated for the specific stand. The default for this parameter is 'YES' (use calibrations) .

## **d. Height-to-Crown Base Calibration (USE HTCB CALIB)**

When a data file is initially entered into ORGANON, height-to-crown base calibrations are calculated for each of the species. If you choose 'YES' for this parameter, the height-to-crown base calibration ratios modify the equations for predicting change in height-to-crown base. If the calibrations were determined from actual tree measurement inputs, the growth models are calibrated for the specific stand. The default for this parameter is 'YES' (use calibrations) .

## **e. Diameter Growth Calibration (USE DIAM. GRO CALIB)**

When a data file is initially entered into ORGANON, diameter growth calibrations are calculated for each of the species. If you choose 'YES' for this parameter, the diameter growth calibration ratios modify the equations for use in diameter growth predictions. If the calibrations were determined from actual tree measurement inputs, the growth models will be calibrated for the specific stand. The system default for this parameter is 'YES' (use calibrations) .

## **f. Limit on Maximum SDI (LIMIT ON MAX. SDI)**

ORGANON has a mortality factor that is applied during each growth cycle. Additional mortality can be placed on a stand by using a self-thinning trajectory approach to a maximum stand density index (Hann and Wang 1990), based on numbers of trees and quadratic mean diameter. The default for this parameter is 'YES' (use limit on maximum SDI).

## **g. Wood Quality Output (WOOD QUALITY OUTPUT)**

If selected with a **Yes**, wood quality information on each cut tree (either from a thinning or a final harvest) is stored on a file specified by the user. When the run is terminated, all residual trees are also added to the wood quality file (i.e., it is assumed that the stand is final harvested at that time). The name of the wood quality file will be requested immediately after the RUN DEFAULTS are finalized, and it will be stored on the specified directory at the end of the run. The wood quality output file can then be used with the TREEVAL program (Ayer-Sachet et al. 1989, Briggs 1989) to analyze the wood quality consequences of the projected management regime (see Maguire et al. 1991 for an example of such a use).

Wood quality output can only be requested for even-aged stands. The format for the wood quality file can be found in Section VIII of this manual.

## **h. Juvenile Wood Core (JUVENILE WOOD CORE)**

This option sets how the juvenile wood core will be defined in the wood quality output. If **Age** is selected, juvenile wood core will be defined as the wood laid down in the first 20 rings at each whorl on the stem. If **Crn** is selected, juvenile wood core will be defined as the wood laid down within the crown (i.e., the wood laid down on all of the rings formed while each whorl was within the crown).

## **i. Printer Form Feed (PRINTER FORM FEED)**

This parameter determines whether there is a form feed (new page) in the output file prior to each report requested. If you do not choose printer form feed, each report may not necessarily start at the top of a new page when printed on the line printer. The default is 'YES' (provide a new page before each report).

## j. Tree List Output (TREE LIST OUTPUT)

If selected with a **yes**, the initial tree list and the tree list at the end of each growth period are stored on a file specified by the user. The name of the tree list output file will be requested immediately after the RUN DEFAULTS are finalized, and it will be stored on the specified directory at the end of the run. The format for the tree list file can be found in Section X of this manual.

## k. Volume Equations (VOLUME EQUATIONS)

Board Foot volumes are determined by selecting a minimum log top diameter, trim allowance, stump height, log length, and minimum log length. Cubic Foot volumes are determined by designating a conifer top diameter, hardwood top diameter and conifer stump height. (See listings 2 and 3 below for definitions). Values of this parameter can be 'OSU' or 'BLM'. The default setting is 'OSU' (use the OSU volume equations).

Selecting the OSU volume equations will initialize board foot and cubic foot parameters with the following values:

### BOARD FOOT

Minimum log top diameter:	6 inches
Trim allowance:	8 inches
Stump height:	0.5 feet
Log length:	32 feet
Minimum log length:	8 feet

### CUBIC FOOT

Conifer top diameter:	0 inches
Hardwood top diameter:	0 inches
Conifer stump height:	0 inches

If you select the OSU volume equations, each of these parameters is displayed and may be redefined.

If you select the BLM volume equations, the following values are used in calculations and cannot be redefined:

BOARD FOOT

Min. log top dia.: 5 inches if DBH  $\leq$  15";

Variable [5+0.1837(DBH-15)]  
if DBH  $>$  15"

Trim allowance: 0.3 feet

Stump height: 1.5 feet

Log length: 16 feet

Minimum log length: 4.1 feet

CUBIC FOOT

Conifer top dia.: 5 inches if DBH  $\leq$  15";

Variable [5+0.1837(DBH-15)]  
if DBH  $>$  15"

Hardwood top dia.: 5 inches if DBH  $\leq$  15";

Variable [5+0.1837(DBH-15)]  
if DBH  $>$  15 inches

Conifer stump ht.: 1.5 feet

## 2. Board Foot Volume Defaults for OSU Equations

### a. Minimum Board Foot Log Top Diameter (LOG TOP DIAM)

This parameter specifies the top inside bark diameter in inches to be used during board foot calculations of volumes for tables and plots. If you select the OSU volume equations, you can choose any minimum top diameter greater than or equal to two-inches.

### **b. Board Foot Trim Allowance (TRIM ALLOWANCE)**

This parameter specifies the amount of log-end trim in inches to be used during board foot calculations of volumes for tables and plots. If you select the OSU volume equations, you can choose any trim allowance.

### **c. Board Foot Stump Height (STUMP HEIGHT)**

This specifies the stump height in feet to be used during board foot calculations of volumes for tables and plots. If you select the OSU volume equations, you can choose any stump height under 4.5 feet.

### **d. Board Foot Log Length (LOG LENGTH)**

This parameter specifies the log length desired in feet to be used during board foot calculations of volumes for tables and plots. If you select the OSU volume equations, you can choose any log length.

### **e. Board Foot Minimum Log Length (MIN LOG LENGTH)**

This parameter specifies the minimum log length acceptable in feet to be used during board foot calculations of volumes for tables and plots. If you select the OSU volume equations, you can choose any minimum log length.

## **3. Cubic Foot Volume Defaults for OSU Equations**

### **a. Cubic Foot Top Diameter ( TOP DIAM (0.0" – 6.0" ) )**

This parameter specifies the top inside bark diameter in inches to be used during cubic foot calculations of volumes for tables and plots. If you select the OSU volume equations, you can choose any value of cubic foot top diameter between 0 and 6 inches.

### **b. Cubic Foot Stump Height (STUMP HT)**

This parameter specifies the stump height in feet for to be used during cubic foot calculations of volumes for tables and plots. If you select the OSU volume equations, you can choose any stump height below 4.5 feet.

## 4. Volume Defaults for BLM Equations

### a. BLM Minimum DBH (BLM MINIMUM DBH)

This parameter specifies the minimum tree DBH for which the BLM volumes will be computed. The parameter must be at least 6.0-inches in size.

### b. BLM Resource Area (BLM RESOURCE AREA)

This parameter specifies the appropriate BLM Resource Area to be used for the BLM volume equation coefficients. The Resource Areas available for SWO-ORGANON include:

<u>Code</u>	<u>Resource Area</u>
344	South Umpqua
351	North Umpqua
352	Drain/Dillard
511	All Medford

The Medford Resource Area (511) is the default value in SWO-ORGANON.

The Resource Areas available for NWO- and SMC-ORGANON include:

<u>Code</u>	<u>Resource Area</u>
144	Clackamas/Molalla/Santiam
172	Alsea/Rickreall/Yamhill
231	McKenzie/South-Valley
243	South-Valley/Coast-Range

The Alsea/Rickeall/Yamhill Resource Area (172) is the default value in NWO- and SMC-ORGANON.

The following example shows the default selection menu when you choose the system defaults, and the OSU volume equations are replaced with BLM volume equations.

DEFAULT SELECTION EXAMPLE

[ DEFAULT INPUT SELECTION ]

1 - Use System Defaults
2 - Use Default file 'ORGANON.DEF'
3 - Create 'ORGANON.DEF'

[ <CR> = Use System Defaults ]

INPUT ---> 1

```

----- [ RUN DEFAULTS ] -----
1.      TRIPLING: Yes
2.      DISPLAY MENUS: Yes
3.      USE HEIGHT CALIB: Yes
4.      USE HTCB CALIB: Yes
5.      USE DIAM. GRO CALIB: Yes
6.      LIMIT ON MAX. SDI: Yes
7.      WOOD QUALITY OUTPUT: No
8.      JUVENILE WOOD CORE: Age
9.      PRINTER FORM FEED: Yes
10.     TREE LIST OUTPUT: No
11.     VOLUME EQUATIONS: OSU

----- [ BOARD FOOT DEFAULTS ] -----
12.     LOG TOP DIAM: 6. inches
13.     TRIM ALLOWANCE: 8. inches
14.     STUMP HEIGHT: .5 feet
15.     LOG LENGTH: 32 feet
16.     MIN LOG LENGTH: 8.0 feet

----- [ CUBIC FOOT DEFAULTS ] -----
17.     TOP DIAM (0.0" - 6.0"): .0 inches
18.                     STUMP HT: .0 feet

----- [ <CR> to end ] -----
INPUT # TO MODIFY ---> 11

```

```

----- [ RUN DEFAULTS ] -----
1.      TRIPLING: Yes
2.      DISPLAY MENUS: Yes
3.      USE HEIGHT CALIB: Yes
4.      USE HTCB CALIB: Yes
5.      USE DIAM. GRO CALIB: Yes
6.      LIMIT ON MAX. SDI: Yes
7.      WOOD QUALITY OUTPUT: No
8.      JUVENILE WOOD CORE: Age
9.      PRINTER FORM FEED: Yes
10.     TREE LIST OUTPUT: No
11.     VOLUME EQUATIONS: BLM

----- [ BLM VOLUME DEFAULTS ] -----
12.     BLM MINIMUM DBH (>= 6.0"): 7.0 inches
13.     BLM RESOURCE AREA: 511
      (344 = SOUTH UMPQUA
      351 = NORTH UMPQUA
      352 = DRAIN/DILLARD
      511 = ALL MEDFORD)

----- [ <CR> to end ] -----
INPUT # TO MODIFY --->

```

To continue the following example in this manual, reset #1 (TRIPLING) from a 'Yes' to a 'No', and reset #11 (VOLUME EQUATIONS) to OSU. The following example shows how to change item nine on the default menu (PRINTER FORM FEED) from a 'YES' to a 'NO', and item twelve (BOARD FOOT LOG TOP DIAMETER) from 6.0 inches to 4.0 inches.

DEFAULT SELECTION EXAMPLE (continued)

```

[ RUN DEFAULTS ]
1.      TRIPLING: No
2.      DISPLAY MENUS: Yes
3.      USE HEIGHT CALIB: Yes
4.      USE HTCB CALIB: Yes
5.      USE DIAM. GRO CALIB: Yes
6.      LIMIT ON MAX. SDI: Yes
7.      WOOD QUALITY OUTPUT: No
8.      JUVENILE WOOD CORE: Age
9.      PRINTER FORM FEED: Yes
10.     TREE LIST OUTPUT: No
11.     VOLUME EQUATIONS: OSU

[ BOARD FOOT DEFAULTS ]
12.     LOG TOP DIAM: 6. inches
13.     TRIM ALLOWANCE: 8. inches
14.     STUMP HEIGHT: .5 feet
15.     LOG LENGTH: 32 feet
16.     MIN LOG LENGTH: 8.0 feet

[ CUBIC FOOT DEFAULTS ]
17. TOP DIAM (0.0" - 6.0"): .0 inches
18.                      STUMP HT: .0 feet

[ <CR> to end ]
INPUT # TO MODIFY ---> 9

```

```

[ RUN DEFAULTS ]
1.      TRIPLING: No
2.      DISPLAY MENUS: Yes
3.      USE HEIGHT CALIB: Yes
4.      USE HTCB CALIB: Yes
5.      USE DIAM. GRO CALIB: Yes
6.      LIMIT ON MAX. SDI: Yes
7.      WOOD QUALITY OUTPUT: No
8.      JUVENILE WOOD CORE: Age
9.      PRINTER FORM FEED: No
10.     TREE LIST OUTPUT: No
11.     VOLUME EQUATIONS: OSU

[ BOARD FOOT DEFAULTS ]
12.     LOG TOP DIAM: 6. inches
13.     TRIM ALLOWANCE: 8. inches
14.     STUMP HEIGHT: .5 feet
15.     LOG LENGTH: 32 feet
16.     MIN LOG LENGTH: 8.0 feet

[ CUBIC FOOT DEFAULTS ]
17. TOP DIAM (0.0" - 6.0"): .0 inches
18.                      STUMP HT: .0 feet

[ <CR> to end ]
INPUT # TO MODIFY ---> 12

```

Enter inches--->4

DEFAULT SELECTION EXAMPLE (continued)

[ RUN DEFAULTS ]	
1.	TRIPPLING: No
2.	DISPLAY MENUS: Yes
3.	USE HEIGHT CALIB: Yes
4.	USE HTCB CALIB: Yes
5.	USE DIAMETER CALIB: Yes
6.	LIMIT ON MAX. SDI: Yes
7.	WOOD QUALITY OUTPUT: No
8.	JUVENILE WOOD CORE: Age
9.	PRINTER FORM FEED: No
10.	TREE LIST OUTPUT: No
11.	VOLUME EQUATIONS: OSU
[ BOARD FOOT DEFAULTS ]	
12.	LOG TOP DIAM: 4. inches
13.	TRIM ALLOWANCE: 8. inches
14.	STUMP HEIGHT: .5 feet
15.	LOG LENGTH: 32 feet
16.	MIN LOG LENGTH: 8.0 feet
[ CUBIC FOOT DEFAULTS ]	
17.	TOP DIAM (0.0" - 6.0"): .0 inches
18.	STUMP HT: .0 feet
[ <CR> to end ]	
INPUT # TO MODIFY ---> <CR>	

Default values are now set.

<CR> to continue to main menu ...

When the all of the defaults have been modified to the desirable values, they can be set for the run by pressing a carriage return (<CR>). If DEFAULT INPUT SELECTION #3 (Create 'ORGANON.DEF') had been selected before modifying the default values, then the new default values will also be stored on file 'ORGANON.DEF' for future use.

## B. **Genetic Worth Values for Douglas-fir**

Genetic worth values can be applied to evenaged stands with at least one Douglas-fir tree. Genetic worth values can be entered in all three versions of ORGANON. There are separate genetic worth values for diameter growth rate and height growth rate. For both, values are expressed in percent and can range from 0.0 to 20.0. A value of 0.0 represents the growth rate of woods-run seed, which is the default value. The following example shows how genetic worth values are entered (in this case, entering the woods-run values of 0.0, which would be unnecessary in a "real" ORGANON run).

DO YOU WISH TO ENTER GENETIC WORTH VALUES  
FOR DOUGLAS-FIR? (N) ---> **Y**

DIAMETER GROWTH RATE GENETIC WORTH (%) = **0.0**

HEIGHT GROWTH RATE GENETIC WORTH (%) = **0.0**

### **C. Impact of Swiss Needle Cast on Douglas-fir**

The impact of Swiss needle cast on the growth of Douglas-fir can be applied to evenaged stands with at least one Douglas-fir tree. The impact of Swiss needle cast is expressed through its effect upon the foliage retention of the trees. A foliage retention value can be entered only in the NWO and SMC versions of ORGANON. Foliage retention values are expressed in decimal years and can range from 0.85 to 7.00. A value of 7.00 represents the maximum number of years that Douglas-fir can retain needles and it is the default value. The impact of Swiss needle cast on Douglas-fir is basically negligible for values over 3.00. The foliage retention value entered is used throughout the ORGANON run by modifying both the diameter growth rate and the height growth rate predictions. The following example shows how a foliage retention value is entered (in this case, entering the maximum foliage retention value of 7.00, which would be unnecessary in a "real" ORGANON run).

```
HAS YOUR DOUGLAS-FIR BEEN INFECTED  
WITH SWISS NEEDLE CAST? (N) ---> Y  
FOLIAGE RETENTION VALUE = 7.00
```

### **D. Wood Quality Output File Name**

If the WOOD QUALITY OUTPUT default #7 has been set to 'Yes', ORGANON will next ask for the name to be used for the wood quality output file. The following example shows the procedure for creating a wood quality output file called '**WOODQUAL.OUT**'.

```
Enter Wood Quality Output File Name ---> WOODQUAL.OUT
```

## ***E. Tree List Output File Name***

If the TREE LIST OUTPUT default #7 has been set to 'Yes', ORGANON will next ask for the name to be used for the tree list output file. The following example shows the procedure for creating a tree list output file called '**TREELIST.OUT**'.

Enter Tree List Output File Name ---> **TREELIST.OUT**

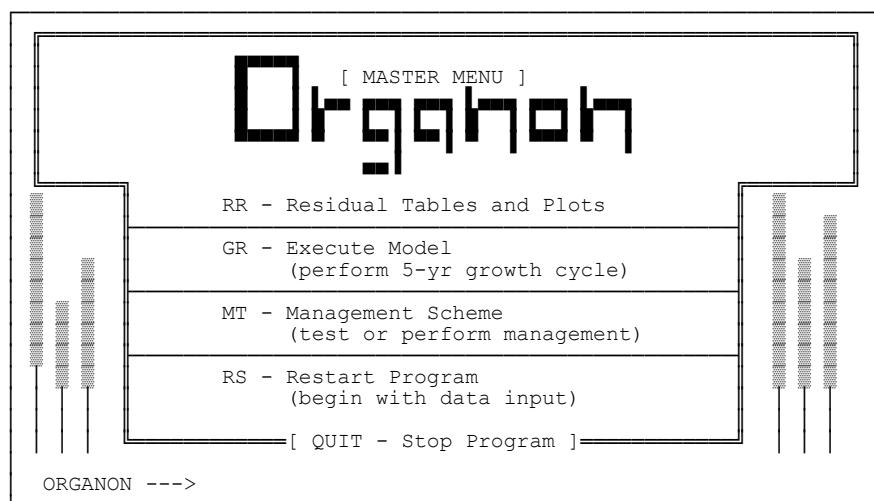
## ***F. Execution Suggestions***

The following tips will make execution of the ORGANON model faster and simpler.

1. In most cases, when ORGANON prompts you for a response, a response appears in parentheses after the prompt. This response is ORGANON's default response should you press a carriage return (<CR>). The values of the default responses (carriage returns) were selected by ORGANON's authors as the most frequently expected responses. Running ORGANON with default responses reduces user keyboard entries and speeds program execution.
2. Whenever ORGANON prompts you for a YES or NO response, entering 'Y', 'y', 'YES', or 'yes' are all acceptable values for yes. The values 'N', 'n', 'NO' or 'no' are acceptable values for no.
3. Any response may be entered in all capital letters or all small letters. ORGANON is not case sensitive.
4. When menus are not displayed, you may request them at any time by entering '?' or 'HELP' when prompted.
5. When a number of reports must be printed, ORGANON runs faster if all report output is to a file only, or to the screen and a file. After program execution, use the DOS 'PRINT' command to print reports in the output file. You may edit the output file with a word processor to eliminate all but the required reports.
6. You should send plots and tables to an output file as well as to the screen. The output file describes the stand and contains all defaults and parameters associated with the stand's requested reports and tables. In addition, ORGANON's run history attached to the end of the output file contains a listing of the management decisions and growth cycles in a management scenario.

## **G. Master Menu Options**

After data are entered, edited, and checked (including selecting defaults), ORGANON comes under the control of the master menu. At that point, ORGANON becomes a 'user-directed' program. This means that a main menu is displayed and you, the user, must select one of five program options (REPORTS, GROWTH, MANAGEMENT, RESTART, QUIT). After you select a run option, ORGANON processes your input and displays the main menu, prompting you to select another run option. The following are all selections that may appear on the main menu. Some selections are only available at certain points during program execution while others are available at all times.



## 1. Table and Plot Parameters

### a. Species

Each time you select certain RESIDUAL or CUT REPORTS from the Master Menu or Management Menu or perform certain thins within the Management Menu, you must also select the species or species group to be reported or thinned. The species choices are listed below.

AL	All Species - Lumps all species listed in section SPECIES CODE NUMBER together
SP	Specific Species - One of the specific species listed in SPECIES CODE NUMBER
AC	All conifers - Lumps all trees with species codes less than or equal to 300 together
AH	All hardwoods - Lumps all trees with species codes greater than 300 together

The selected species or species group is fixed until you exit the REPORT menu. The default response (<CR>) for the species codes is 'AL', ALL SPECIES. The following examples show how to select reports for display of a species group (ALL HARDWOODS), and a single species (DOUGLAS-FIR).

#### SPECIES SELECTION EXAMPLE #1

Species groups: AL - All Species AC - All Conifers AH - All Hardwoods	Specific Species: DF - DOUGLAS FIR PP - PONDEROSA PINE IC - INCENSE CEDAR MD - MADRONE TA - TANOAK BL - BIG LEAF MAPLE BO - CAL. BLACK OAK PD - PACIFIC DOGWOOD	GW - GRAND/WHITE FIR SP - SUGAR PINE WH - WESTERN HEMLOCK GC - CHINKAPIN CL - CANYON LIVE OAK WO - ORE. WHITE OAK RA - RED ALDER WI - WILLOW
--	---	---

SPECIES OR SPECIES GROUP DESIRED (AL) ----> AH

#### SPECIES SELECTION EXAMPLE #2

Species groups: AL - All Species AC - All Conifers AH - All Hardwoods	Specific Species: DF - DOUGLAS FIR PP - PONDEROSA PINE IC - INCENSE CEDAR MD - MADRONE TA - TANOAK BL - BIG LEAF MAPLE BO - CAL. BLACK OAK PD - PACIFIC DOGWOOD	GW - GRAND/WHITE FIR SP - SUGAR PINE WH - WESTERN HEMLOCK GC - CHINKAPIN CL - CANYON LIVE OAK WO - ORE. WHITE OAK RA - RED ALDER WI - WILLOW
--	---	---

SPECIES OR SPECIES GROUP DESIRED (AL) ----> DF

## b. Destination

When you request any reports, you must also choose a destination for those tables and plots. That destination holds for every plot or table requested until you exit the report menu. When you next display the report menu, ORGANON again requests the destination for tables and plots. Destination choices for tables and plots can include any in the following list.

SO - Screen only

PO - Printer only

SF - Screen and file

The default response for a destination is 'SO', SCREEN ONLY. The following example chooses a report destination of 'FO', FILE ONLY. The report does not display on the screen, but is only written to the output file (TESTOUT in this case) that you selected at the start of the ORGANON run.

### DESTINATION SELECTION EXAMPLE

Would you like these reports displayed on:

SO - Screen Only  
FO - File: TESTOUT  
SF - Screen  
and File: TESTOUT

DISPLAY (SO) ---> **FO**

### c. Windows

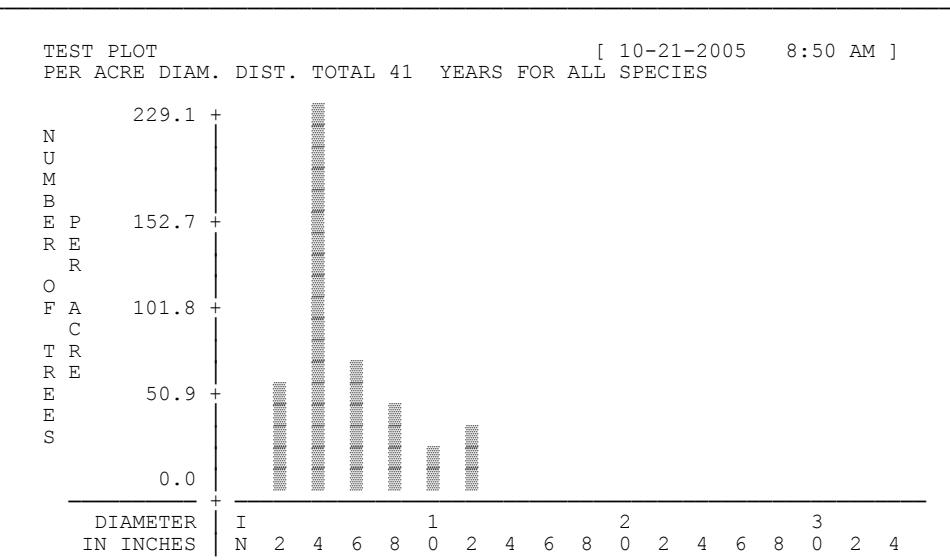
You can request a window for any plot selected. The window determines the 2" diameter classes to be included in the display. The default response for windows is 'N' (NO window selection), which displays the entire diameter class scale from 0" to 36". If a window is desired, a 'Y' response requires input of an even number minimum and maximum (within the 0"-36" limit) diameter class to be displayed. Values for all diameter classes outside the specified window are not displayed. Window selection forces a rescaling of the Y-axis values of the plot and results in a more accurate display of the requested diameter classes. This feature is particularly useful when one (or several) diameter class(es) has a very large value compared to the other diameter classes in the plot. As a result, the other classes may appear to have the same value. By using the window option, very large value(s) can be eliminated from the plot. This allows you to inspect the remaining classes in more detail. If you select a window to plot, a description below the diameter class X-axis indicates the range requested. This description will appear on plots to all destinations except the screen.

Under no circumstances are diameter classes greater than 36" displayed. A message appears identifying the number of trees greater than 36" in diameter that do not appear on that plot.

ORGANON prompts you for window selection input each time you request a plot. Windowing gives you multiple views of the same plot. An example of a screen display of diameter class windows follows.

WINDOW SELECTION EXAMPLE #1

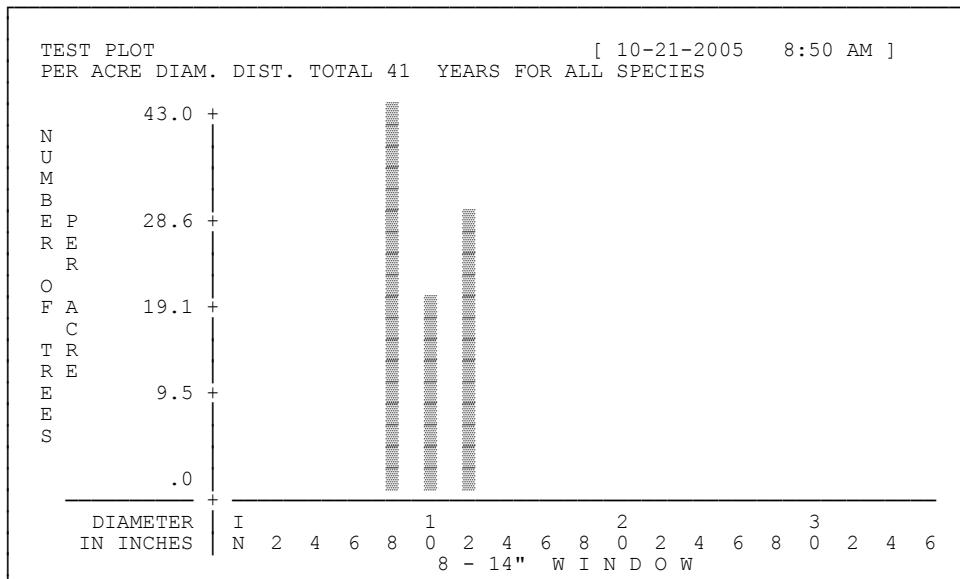
RESIDUAL REPORTS ---> <b>PDF</b>
Window ? (N) ---> <b>&lt;CR&gt;</b>



## WINDOW SELECTION EXAMPLE #2

RESIDUAL REPORTS ---> **PDF**

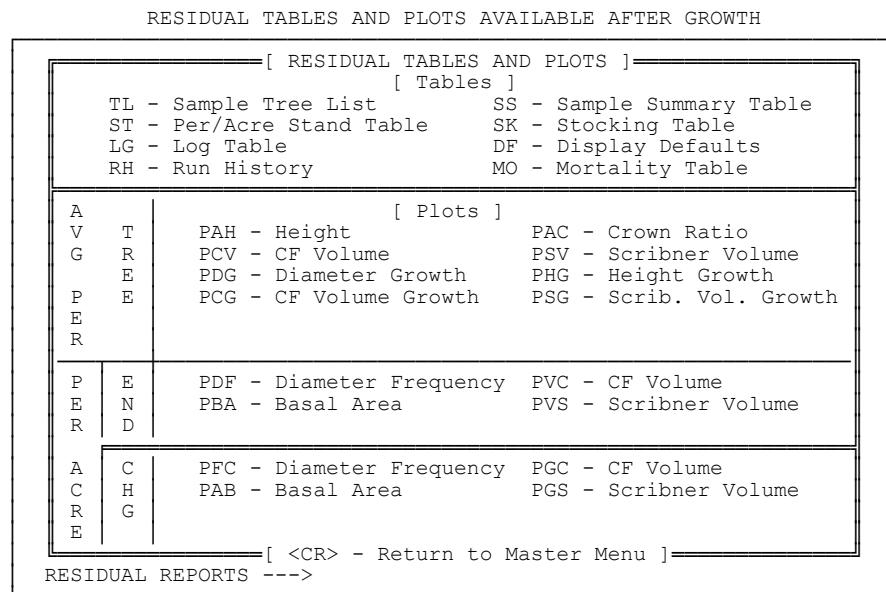
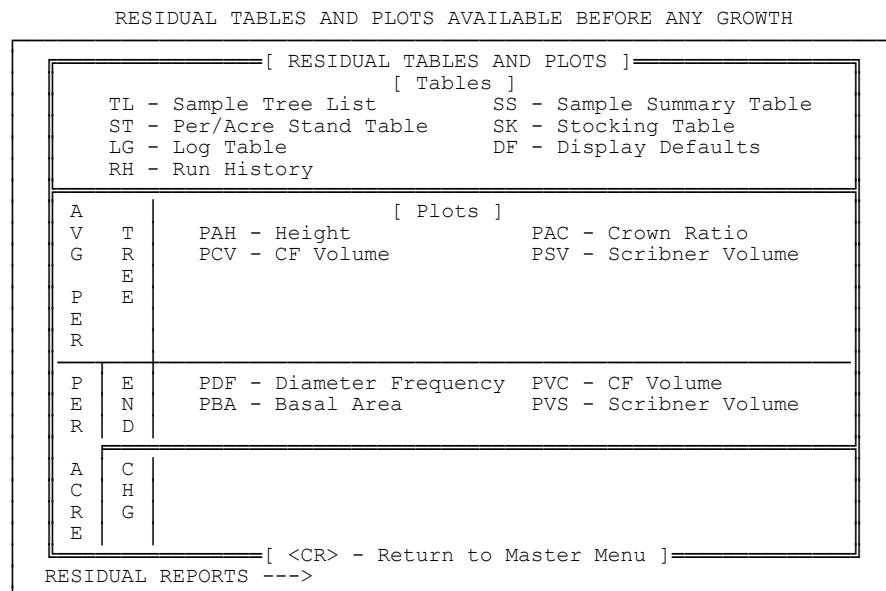
```
Window ? (N) ---> Y
Enter even integer diameter classes between 2 and 36...
Min ---> 8
Max ---> 14
```



NOTE: Window designation at bottom of example will not display on screen output.

## 2. Residual Tables and Plots (RR)

Residual Reports are available at any time on the main menu except immediately following management. Residual Reports display the current residual stand statistics. Residual Reports available within the Management Menu reflect the stand prior to any cut requests (See TRIAL VS ACCEPTED MANAGEMENT). The following examples show the reports and plots available from the Residual Report Menu.



## a. Sample Tree List (TL)

The Sample Tree List Report is a listing of the status of the input sample trees. The header provides the stand identification, age, total stand basal area, number of sample trees and species group. When displaying large sample stands, you may request a report to display the list with a skip factor (i.e., every other tree, every fifth tree, etc.). This allows you to quickly inspect very large data files.

ORGANON displays most items from the sample tree list in the same format as initially entered. However, species, expansion factor and radial growth have been transformed to a form compatible with the growth model. ORGANON changes input species code numbers to alpha codes for ease of reading. ORGANON changes expansion factors to a per acre basis (divided by number of plots/points). ORGANON changes radial growth, if entered, to diameter growth. The following table shows an initial Sample Tree List.

SAMPLE TREE LIST EXAMPLE

TEST PLOT [ 10-21-2005 8:46 AM ]								Page 1
TREE LIST TOTAL 36 YEARS FOR ALL SPECIES -- SKIP=1								
TOTAL SAMPLE TREES = 19 TOTAL STAND BASAL AREA = 65.8								
*****								
TREE	SP	DBH	HT	HTCB	CR	EXP	+HT	+D UC
1	DF	7.8	43.3	11.7	.73	14.32	.0	.00 0
2	DF	11.1	45.9	2.8	.94	7.44	.0	.00 0
3	DF	9.0	40.2	4.4	.89	11.32	.0	.00 0
4	DF	11.1	54.3	.5	.99	7.44	.0	.00 0
5	DF	4.9	35.6	.7	.98	14.32	.0	.00 0
6	DF	3.3	21.9	3.1	.86	57.27	.0	.00 0
7	DF	3.0	19.8	3.0	.85	57.27	.0	.00 0
8	DF	10.4	45.0	5.4	.88	8.48	.0	.00 0
9	DF	9.8	46.6	4.2	.91	9.55	.0	.00 0
10	DF	11.6	58.3	2.9	.95	6.81	.0	.00 0
11	DF	4.1	31.2	3.4	.89	14.32	.0	.00 0
12	DF	7.6	43.6	3.5	.92	14.32	.0	.00 0
13	DF	4.4	30.4	2.4	.92	14.32	.0	.00 0
14	DF	4.6	35.3	9.5	.73	14.32	.0	.00 0
15	DF	.2	5.2	.7	.87	57.27	.0	.00 0
16	DF	6.3	36.7	2.9	.92	14.32	.0	.00 0
17	DF	3.6	20.2	1.0	.95	57.27	.0	.00 0
18	DF	3.9	22.5	.4	.98	57.27	.0	.00 0
19	DF	5.1	30.7	1.5	.95	14.32	.0	.00 0

## b. Sample Summary Table (SS)

The Sample Summary Table provides a condensed version of the Sample Tree List averaged by 2-inch diameter class. This information is averaged sample data--NOT per acre values! The table also displays cubic foot and scribner volume, and cubic foot and scribner volume growth for the average tree in each diameter class. Values for each diameter class displayed in the Sample Summary Table include the upper diameter, but not the lower diameter. The following example shows an initial Sample Summary Table.

SAMPLE SUMMARY TABLE EXAMPLE

TEST PLOT			[ 10-21-2005 8:46 AM ]						Page 1		
INITIAL SAMPLE SUMMARY TABLE AT 36 YEARS FOR ALL SPECIES											
TABLE GROWTH FOR THE PREVIOUS 0 YEARS											
A V E R A G E P E R T R E E											
DIAM CLASS	DBH	HT CR	DIAM GROW	HT GROW	CF VOL	CF GROW	SCRIB VOL	SCRIB GROW			
0 - 2"	.2	5.2	.87	.00	.00	.0	.0	0.	0.	0.	
2 - 4"	3.4	21.1	.91	.00	.00	.6	.0	0.	0.	0.	
4 - 6"	4.6	32.6	.89	.00	.00	1.6	.0	0.	0.	0.	
6 - 8"	7.2	41.2	.86	.00	.00	4.6	.0	13.	0.		
8 - 10"	9.4	43.4	.90	.00	.00	7.7	.0	17.	0.		
10 - 12"	11.0	50.9	.94	.00	.00	12.1	.0	24.	0.		

### c. Per Acre Stand Table (ST)

The Stand Table provides per acre values for number of trees, basal area, cubic foot volume, scribner volume and changes to these values by 2-inch diameter class. If you choose to display all species (AL), the number of trees, basal area, and cubic foot volume are calculated for all species. Scribner volume is calculated for conifer species only. The change values reflect movement from one class to another, mortality, and growth. The following examples show an Initial Stand Table and a Stand Table after 5 year's growth (1 growth cycle).

INITIAL PER ACRE STAND TABLE EXAMPLE

TEST PLOT [ 10-21-2005 8:46 AM ]				Page 1			
INITIAL PER ACRE STAND TABLE AT 36 YEARS FOR ALL SPECIES							
DIAM CLASS	E N D I N G			NET 0-YEAR CHANGE			SCRIB VOL
	TREES/ ACRE	CF BA	SCRIB VOL	TREES/ ACRE	CF BA	SCRIB VOL	
0 - 2"	57.3	.0	0.	0.			
2 - 4"	229.1	15.0	142.	0.			
4 - 6"	71.6	8.4	112.	0.			
6 - 8"	43.0	12.4	197.	571.			
8 - 10"	20.9	10.0	158.	357.			
10 - 12"	30.2	20.0	362.	701.			
TOTALS	451.9	65.8	970.	1628.			

PER ACRE STAND TABLE EXAMPLE

TEST PLOT [ 10-21-2005 8:47 AM ]				Page 1			
PER ACRE STAND TABLE AT 41 YEARS FOR ALL SPECIES							
DIAM CLASS	E N D I N G			NET 5-YEAR CHANGE			SCRIB VOL
	TREES/ ACRE	CF BA	SCRIB VOL	TREES/ ACRE	CF BA	SCRIB VOL	
0 - 2"	53.9	0.2	2.	0.	-3.4	0.2	2.
2 - 4"	.0	0.0	0.	0.	-229.1	-15.0	-142.
4 - 6"	266.1	35.2	485.	780.	194.6	26.8	373.
6 - 8"	42.5	11.6	204.	613.	-0.4	-0.7	8.
8 - 10"	28.4	13.4	275.	615.	7.6	3.4	117.
10 - 12"	20.8	14.4	281.	570.	-9.4	-5.6	-80.
12 - 14"	30.1	28.4	615.	1512.	30.1	28.4	615.
TOTALS	441.9	103.2	1862.	4090.	-10.0	37.5	892.
							2462.

## d. Stocking Table (SK)

The Stocking Table provides the same per acre values displayed in the stand table, only summarized by species group. Additionally, this table provides Reineke's (1933) stand density index (SDI); relative density index, which is the SDI for the stand divided by the maximum SDI the stand's species mix and for the variant being used (Hann and Wang 1990); quadratic mean diameter; the mean height, diameter and crown ratio for all trees greater than 4.5 feet in height; and the estimated crown closure (calculated from the sum of the percent largest crown areas using the formula in Crookston and Stage 1999). The following examples show an initial Stocking Table and a Stocking Table after 5 year's growth (1 growth cycle).

INITIAL RESIDUAL STOCKING TABLE EXAMPLE

RESIDUAL STOCK TABLE															
TEST PLOT				[ 10-21-2005 8:46 AM ]											
DATA FILE: TESTPLOT		*****													
*****															
SPECIES	AT	TREES/	CF	SCRIB	TREES/	CF	SCRIB								
	YR	ACRE	BA	VOL	ACRE	BA	VOL		VOL						
*****															
Doug Fir	36	451.9	65.8	970.	1628.			0-YR CHANGE							
TOTAL:		451.9	65.8	970.	1628.										
Stand Density Index: 157.					Relative Density Index: .295										
Quadratic Mean Diameter: 5.2					Height of 40 Largest: 48.7										
Mean Diameter: 4.4					Mean Crown Ratio: .899										
Estimated % Crown Closure: 68.0															

RESIDUAL STOCKING TABLE EXAMPLE

RESIDUAL STOCK TABLE															
TEST PLOT				[ 10-21-2005 8:46 AM ]											
DATA FILE: TESTPLOT		*****													
*****															
SPECIES	AT	TREES/	CF	SCRIB	TREES/	CF	SCRIB								
	YR	ACRE	BA	VOL	ACRE	BA	VOL		VOL						
*****															
Doug Fir	41	441.9	103.2	1862.	4060.	-10.0	37.5	892.1	2461.8						
TOTALS:		441.9	103.2	1862.	4060.	-10.0	37.5	892.1	2462.						
Stand Density Index: 224.					Relative Density Index: .422										
Quadratic Mean Diameter: 6.5					Height of 40 Largest: 60.6										
Mean Diameter: 5.8					Mean Crown Ratio: .767										
Estimated % Crown Closure: 76.1															

## e. Log Table (LG)

The Residual Log Table provides a gross standing log inventory based on the log parameters selected in the default menu. All conifer trees are divided into logs and then the logs are tallied by species group and top diameter. Volumes for each log are computed using the Columbia Bureau Scribner Log Factors. Also given are a set of totals by species, where average volume is calculated by dividing the total volume by the total number of logs. Values for each diameter class displayed in the Stand Table include the upper diameter, but not the lower diameter. The following example shows a Residual Log Table.

RESIDUAL LOG TABLE EXAMPLE

RESIDUAL LOG TABLE (TOTAL 36 YEARS)									
TEST PLOT		[ 10-21-2005 8:46 AM ]							
LOG LENGTH: 32 feet			MIN LOG LENGTH: 8.0 feet			TOP DIAM: 4.0 inches			
Top Diameter		Doug Logs	Fir Vol	G/W Logs	Fir Vol	P/S Logs	Pine Vol	Other Conifer Logs	Vol
4 - 6"		94.0	1628.2	.0	.0	.0	.0	.0	.0
T O T A L S									
Logs:		94.0		.0		.0		.0	
Volumes:		1628.2		.0		.0		.0	
AVG VOLUME:		17.3		.0		.0		.0	

## f. Sampling Statistics Table (SA)

The Sampling Statistics Table is only available for those '.INP' files in which multiple sampling points/plots were measured. Furthermore, the Sampling Statistics Table is only available at growth cycle 0 (i.e., before any growth projections have occurred). The Sampling Statistics Table provides the mean, standard error of the mean (SE) and the coefficient of variation (CV), in percent, for cubic foot volume per acre and Scribner board foot volume per acre. These values are displayed by species group and across all species.

SAMPLING STATISTICS TABLE EXAMPLE

S A M P L I N G S T A T I T I C S T A B L E					
TEST PLOT	[ 10-21-2005 8:46 AM ]				
DATA FILE: TESTPLOT					
CUBIC FOOT VOLUME:	BOARD FOOT VOLUME:				
Conifer Top Diameter = .0 inches	Top Diameter = 6.0 inches				
Conifer Stump Height = .0 feet	Stump Height = .5 feet				
Hardwood Top Height = .0 inches	Trim Allowance = 8. inches				
	Log Length = 32 feet				
	Minimum Log Length = 8.0 feet				
*****					
SPECIES		CUBIC FOOT VOLUME/ACRE	SCRIBNER BOARD FOOT VOLUME/ACRE		
MEAN		SE	MEAN	SE	CV
*****		*****	*****	*****	*****
Doug Fir	970.	393.	81.0	1628.	794.
TOTALS:	970.	393.	81.0	1628.	794.
*****					
Number of Sample Points = 4					
SE = Standard Error of the Mean					
CV = Coefficient of Variation in Percent					

## g. Mortality Table (MO)

The Mortality Table provides the per acre mortality rate in number of trees, basal area, cubic foot volume and scribner volume that occurred during the last total growth period (one or more specified cycles) for each 2" diameter class. The Mortality Table is only available after one or more growth projections have been made. The mortality rates for multiple cycle growth periods are the sum of the mortality rates calculated in each cycle. The diameter classes of the table are determined by the diameters at the start of each growth cycle. Likewise, basal area and volumes in mortality are based upon tree characteristics at the start of each cycle. The underlying assumption in ORGANON is that mortality trees have no growth just prior to death. The following example shows a mortality table after one growth cycle.

MORTALITY TABLE EXAMPLE

TEST PLOT		[ 10-21-2005 8:46 AM ]		Page	1
MORTALITY TABLE AT 41 YEARS FOR ALL SPECIES					
DIAM CLASS	TREES/ ACRE	5-YEAR MORTALITY RATE			SCRIB VOL
		CF	VOL	VOL	
0 - 2"	3.36	0.00	0.00	0.00	
2 - 4"	5.13	0.32	3.01	0.00	
4 - 6"	1.07	0.12	1.65	0.00	
6 - 8"	0.32	0.09	1.46	4.24	
8 - 10"	0.08	0.04	0.58	1.31	
10 - 12"	0.06	0.04	0.70	1.36	
TOTALS	10.02	0.61	7.40	6.91	

## **h. Run History (RH)**

The Run History report is available at any time on-screen and is included on the output file after QUIT or RESTART. Run History is also available within the Management Menu. This report contains the current status and history of the ORGANON run. This includes present stand age, current cycle and previous stand activities. If management is in progress, trial cuts are displayed (See TRIAL VS ACCEPTED MANAGEMENT). The following example shows a Run History report while management is in progress after previous stand growth and management.

RUN HISTORY EXAMPLE

```
RUN HISTORY AND STATUS
Southwest Oregon Version, Edition 9.0
[ 10-21-2011 8:46 AM ]

TEST PLOT
Growth Cycles Completed: 3
Breast Height Stand Age: 43
Total Stand Age: 51
Douglas-fir Site Index: 109.4
Ponderosa Pine Site Index: 102.9
Status: TRIAL MGMT

RUN HISTORY
*****
YEAR ACTIVITY
*****
36 GROWTH --> 1 CYCLE
41 THIN BA (AL) from above --> 85.1 resid. sq ft
41 THIN DBH (AL) 0 " -->50 % 75 " -->50 %
41 GROWTH --> 2 CYCLES

Trial Management in progress...

SDI THIN proportional --> Target 100

<CR> to continue...
```

## i. Display Defaults (DF)

This selection displays the current settings for the run, and board foot and cubic foot default parameters as described in the section ORGANON PROGRAM DEFAULTS AND SPECIFICATIONS. DISPLAY DEFAULTS is only available on-screen.

DISPLAY DEFAULTS EXAMPLE

[ RUN DEFAULTS ]	
1.	TRIPLING: No
2.	DISPLAY MENUS: Yes
3.	USE HEIGHT CALIB: Yes
4.	USE HTCB CALIB: Yes
5.	USE DIAMETER CALIB: Yes
6.	LIMIT ON MAX. SDI: Yes
7.	WOOD QUALITY OUTPUT: No
8.	JUVENILE WOOD CORE: Age
9.	PRINTER FORM FEED: No
10.	TREE LIST OUTPUT: No
11.	VOLUME EQUATIONS: OSU
[ BOARD FOOT DEFAULTS ]	
12.	LOG TOP DIAM: 6. inches
13.	TRIM ALLOWANCE: 8. inches
14.	STUMP HEIGHT: .5 feet
15.	LOG LENGTH: 32 feet
16.	MIN LOG LENGTH: 8.0 feet
[ CUBIC FOOT DEFAULTS ]	
18.	TOP DIAM (0.0" - 6.0") : .0 inches
19.	STUMP HT: .0 feet
[ <CR> to end ]	

The following values are then displayed if they had been chosen by the user:

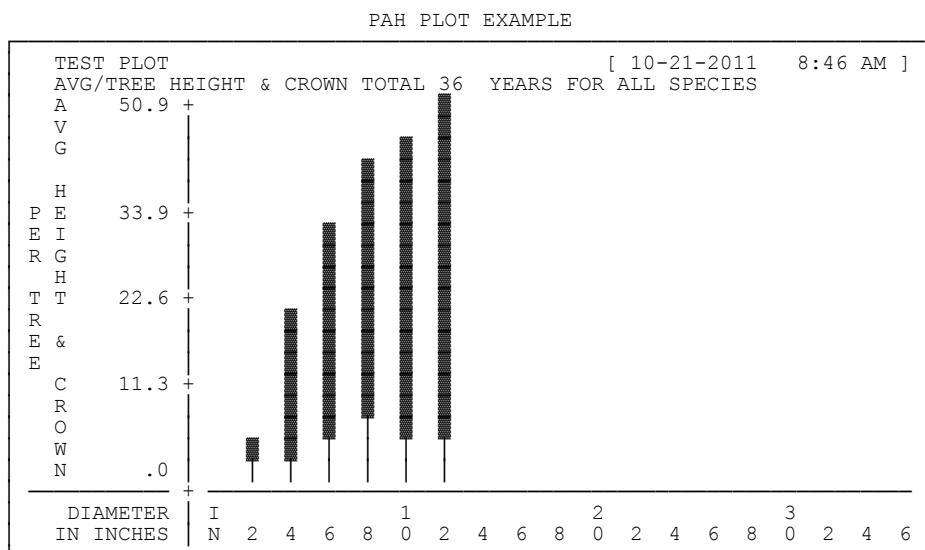
DIAMETER GROWTH RATE GENETIC WORTH (%) = 0.0
HEIGHT GROWTH RATE GENETIC WORTH (%) = 0.0
SWISS NEEDLE CAST FOLIAGE RETENTION VALUE = 7.00

## j. Average Plots

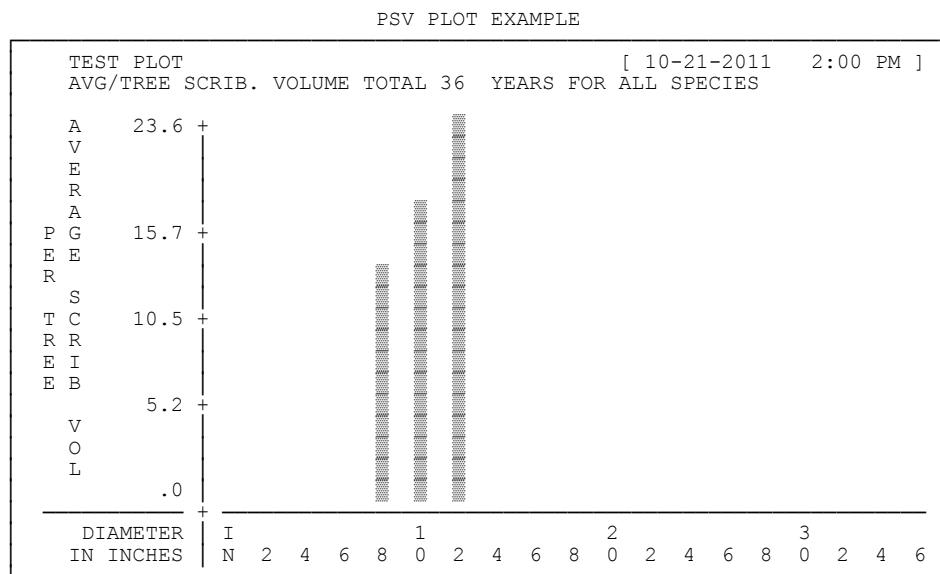
For average variables displayed in the Sample Summary Table, there is a corresponding plot of that variable by diameter class. The diameter values displayed on the X-axis indicate the upper diameter of the class (i.e., 14 represents 12" < DBH ≤ 14"). The following table shows the plots available associated with the Sample Summary Table.

TABLE: Residual Sample Summary	
ASSOCIATED PLOTS:	PAH      Average Height PAC      Average Crown Ratio PDG      Average Diameter Growth PHG      Average Height Growth PCV      Average Cubic Foot Volume PSV      Average Scribner Volume PCG      Average Cubic Foot Volume Growth PSV      Average Scribner Volume Growth

The following example is a PAH plot showing a stand profile by plotting average tree height and average crown base by diameter class. The 'IN' diameter indicates ingrowth trees and will only display during trial management (see MANAGEMENT INGROWTH).



The following PSV plot is a histogram of average scribner volume for the trees in each diameter class.

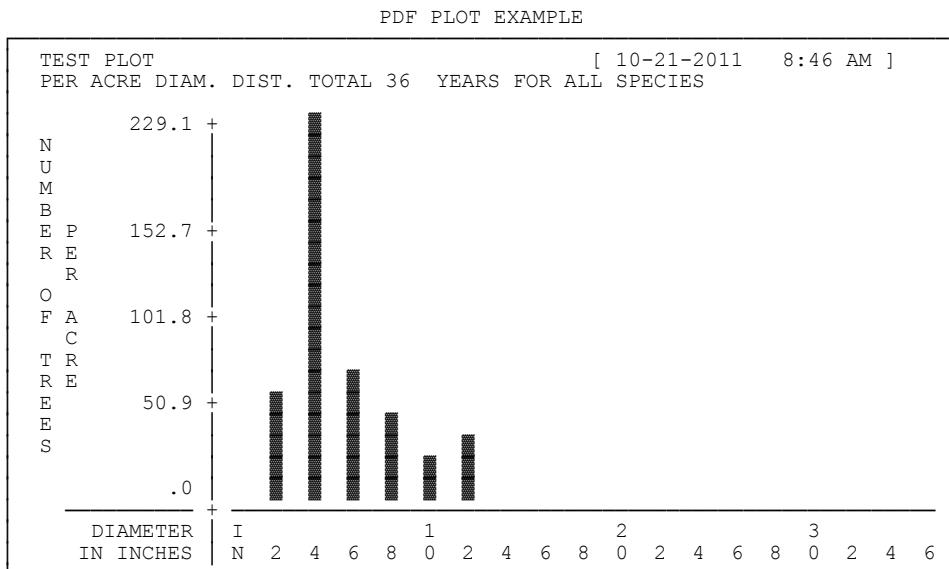


## k. Per Acre Plots

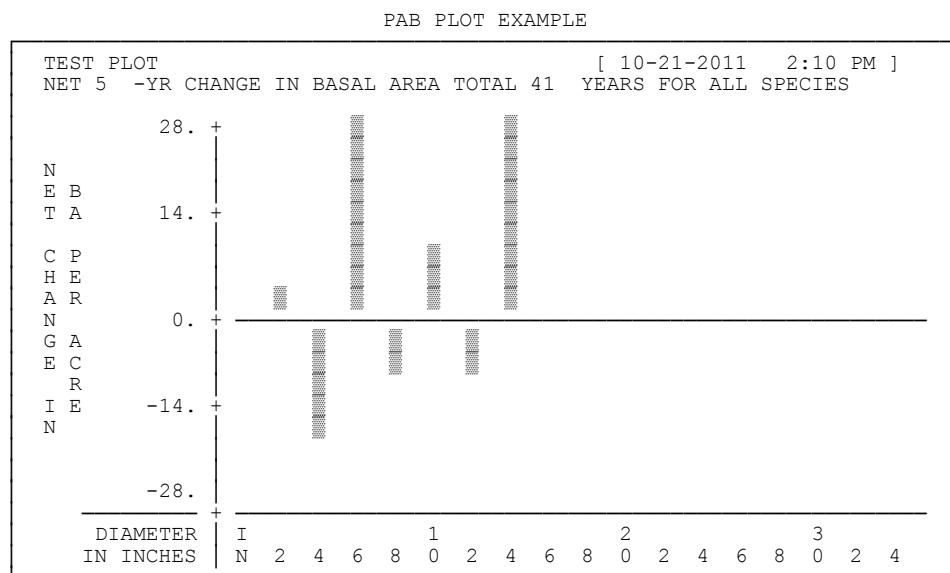
For any per acre variable displayed on the Stand Table, ORGANON can plot that variable by diameter class. The diameter values displayed on the X-axis indicate the upper diameter of the class (i.e., 14 represents 12" < DBH £ 14"). The following table shows the plots available associated with the Stand Table.

TABLE: Residual Stand Table	
ASSOCIATED PLOTS:	PDF Ending Diameter Frequency PBA Ending Basal Area PVC Ending Cubic Foot Volume PVS Ending Scribner Volume PFC Change in Diameter Frequency PAB Change in Basal Area PGC Change in Cubic Foot Volume PGS Change in Scribner Volume

The following is a PDF plot example which is a histogram of the per acre diameter distribution.



The following example is a PAB plot which is a histogram of the per acre basal area change by diameter class for the last set of growth cycles requested.



### 3. Growth (GR)

#### a. Growth Cycles

GROWTH CYCLES are conducted in five-year cycles for the SWO, NWO, and SMC versions of ORGANON. The RAP version of ORGANON uses an annual growth period. In a growth cycle, tree height growth, diameter growth, mortality, and crown change all take place. If requested, tripling and yield table output can also be done. You can choose any number of growth cycles, as long as the total number does not exceed the growth cycle limits as explained in the next section. REPORTS and MANAGEMENT are only available after completion of the number of growth cycles requested. Because they are automatic and not user-selected, yield tables are the only tables available at each growth cycle regardless of the number of growth cycles that you request. After all growth cycles selected are complete, ORGANON displays all main menu options. The following is an example where the stand is grown for three cycles.

#### GROWTH CYCLE EXAMPLE

```
ORGANON ---> GR
```

```
Number of 5-year cycles to execute (<CR> = 1, 0 = NO GROWTH) ? ---> 3
```

```
[ execution beginning ]
```

```
CYCLE 1 -- COMPUTATION ENDS WITH 5 YEARS TOTAL STAND GROWTH
```

```
CYCLE 2 -- COMPUTATION ENDS WITH 10 YEARS TOTAL STAND GROWTH
```

```
CYCLE 3 -- COMPUTATION ENDS WITH 15 YEARS TOTAL STAND GROWTH
```

## b. Growth Cycle Limits

A warning message will be displayed grown when more than 50% of the major species in the stand reach a maximum growth effective age. For SWO-ORGANON, the major species are Douglas-fir, Grand/White Fir, Incense Cedar, Ponderosa Pine, and Sugar Pine and the maximum growth effective age is 500 breast-height years. For NWO-ORGANON, the major species are Douglas Fir and Grand Fir and the maximum growth effective age is 120 breast-height years. For SMC-ORGANON, the major species are Douglas Fir and Western Hemlock and the maximum effective age is 120 breast-height years. For RAP-ORGANON, the major species is red alder and the maximum effective age is 25 total years from seed. No growth can occur after all of the major species in the stand have died or have been cut. Finally, no growth can occur after the stand has been FINAL HARVESTED.

### GROWTH CYCLE LIMITS EXAMPLE #1

```
ORGANON ---> GR
```

```
NO GROWTH CYCLES POSSIBLE -- NO REMAINING MAJOR SPECIES
```

### GROWTH CYCLE LIMITS EXAMPLE #2

```
ORGANON ---> GR
```

```
Number of 5-year cycles to execute? (1) ---> 110
```

```
CYCLE 99 -- COMPUTATION ENDS WITH 495 YEARS TOTAL STAND GROWTH
```

```
CYCLE 100 -- COMPUTATION ENDS WITH 500 YEARS TOTAL STAND GROWTH
```

```
----- WARNING -----
```

```
A MAJORITY OF THE STAND IS OVER 500 YEARS BH AGE!!!!
```

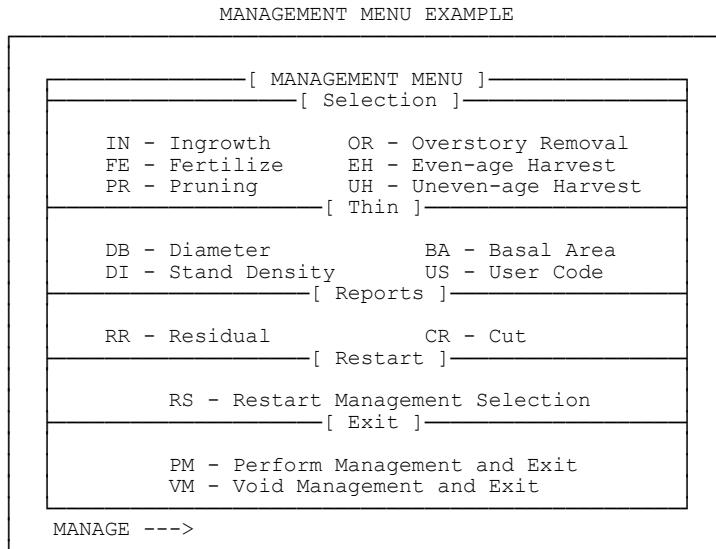
```
FUTURE PREDICTIONS ARE EXTRAPOLATIONS!!!!
```

```
<CR> to continue...
```

NOTE: The preceding examples do not necessarily reflect messages given for example TEST PLOT

## 4. Management (MT)

The management routines let you select, view and execute a management scheme incorporating one or more of the following options: (1) adding ingrowth to the stand, (2) removing overstory trees from the stand, (3) fertilizing the stand, (4) conducting an even-aged harvest, (5) pruning trees in the stand, (6) conducting an uneven-aged harvest, and (7) thinning the stand. A display of the Management Menu follows.



## a. Creating a Management Scheme ('LAYERED' MANAGEMENT)

All management options are performed in a 'layered' fashion. A number of management options are available, and you can choose any number of them with their effects added to previous management decisions. As a result, a cumulative management scheme is performed. This allows you to design any manner of thinning desired. The stand may be viewed via REPORTS at any point while the management scheme is being built. If too much has been cut, you can choose RESTART to begin again. If not enough has been cut, you can choose a new 'layer' of thinning to increase the cut. Because of this 'building' scheme, ORGANON prompts you to verify each thinning decision to avoid possible re-entry of a multilayer thin due to typing error. The following example shows thinning of all mistletoe trees marked as user code 1 using 'User Code Thin' (US) and 50% of all hardwoods under 10" using 'Diameter Thin' (DB).

### CREATING A MANAGEMENT SCHEME EXAMPLE

MANAGE ---> **US**

Enter user code to thin ---> **1**  
Enter percent to cut ---> **100**  
Accept this thin (Y) ? ---> <CR>

MANAGE ---> **DB**

SPECIES OR SPECIES GROUP DESIRED (AL) ---> <CR>

[ \*\*\* WARNING \*\*\* ]  
Lower DBH value 'not' included...  
Upper DBH value included...  
(i.e. lower < CUT <= upper)

Enter lower DBH ---> **0**  
Enter lower removal % ---> **50**  
Enter upper DBH ---> **10**  
Enter upper removal % ---> **50**

Accept this thin (Y) ? ---> <CR>

MANAGE ---> **PM**

## **b. Trial vs Accepted Management**

As the construction of a management scheme is progressing by 'layering', each thinning is being performed on a trial basis. This means the stand has not actually been changed. A new layer of management can be added until the final result has been achieved. All cut reports viewed at this time are labeled as 'TRIAL' only. When the management is satisfactory, the 'TRIAL' cut can only become permanent by specifically designating acceptance. The acceptance (PM - PERFORM MANAGEMENT) takes you out of the management menu back to the main menu. If unacceptable, a decision to void the management and return the stand back to its original condition (VM - VOID MANAGEMENT) also exits management and sends you back to the main menu. To void the management but remain in the management menu for another try, choose RESTART. After you leave management by choosing 'PM', MANAGEMENT no longer is available from the master menu until after the next growth cycle. If you choose a VM exit from management, MANAGEMENT is still available from the master menu.

## **c. Management Selection**

### **1. *Ingrowth (IN)***

Ingrowth selection from the management menu allows the addition of small trees to the tree list. Expansion factors (i.e., the number of trees per acre the ingrowth tree represents) will not be adjusted in any way and must be input for the stand. Ingrowth can be added to the stand by reading either an existing ingrowth tree list file or by directly entering the ingrowth trees through the keyboard.

#### **a. Existing File Input**

An existing ingrowth file can be created by using either a word processor or by first entering the trees through the keyboard in ORGANON and then saving the file.

You can use any word processor that generates an ASCII file to create the data file. An ASCII file is a file that contains no formatting characters (word wrap, formatting, etc.). This is generally referred to as a flat, or non-document file. Wordstar, WordPerfect, MS-Word, MS-DOS Edit, or MS-Windows NotePad can create this type of file. Check your word processor manual for instructions on creating an ASCII file.

Use one line (all characters up to a carriage return) to enter all the data for one tree. The total number of lines in the file should equal the total number of trees being entered.

All data elements should be right justified in their field. If an optional element is not included, enter blanks in its field. In the following description, an integer refers to a whole number (no decimal point, i.e., 365). A real number implies a decimal number (i.e., 27.4).

Element	Col #	Comment
1	1-3	Species Code number (INTEGER). REQUIRED. One of the 3-digit codes from section SPECIES CODE NUMBER. (e.g., 202)
2	5-9	Diameter Outside Bark at Breast Height in inches (REAL-1 decimal place). REQUIRED. (e.g., 27.5)
3	11-15	Total Tree Height in feet (REAL-1 decimal place). STRONGLY RECOMMEND (5 blanks if omitted). (e.g., 134.9)
4	17-20	Crown Ratio (REAL-2 decimal places). STRONGLY RECOMMEND (4 blanks if omitted). (e.g., .63)
5	22-27	Expansion Factor [trees per acre the ingrowth tree represents] (REAL-2 decimal places). REQUIRED. (e.g., 25.24)
6	29-30	User Code (INTEGER). Any designated identification number for user specified thinning. OPTIONAL (2 blanks if omitted). (e.g., 2)

The following example shows the procedure for adding ingrowth trees to a stand using an existing ingrowth file called '**INGROWTH.DTA**'.

INGROWTH EXAMPLE #1

MANAGE ---> **IN**

INGROWTH EXAMPLE #1 (continued)

```
Do you wish to use an existing ingrowth file (N)? Y
Enter ingrowth tree data file name
---> INGROWTH.DTA
```

b. Keyboard Input

The following example shows the procedure for adding ingrowth trees to a stand by entering them through the keyboard.

INGROWTH EXAMPLE #2

```
MANAGE ---> IN
```

```
Do you wish to use an existing ingrowth file (N)? N
```

```
[ INGROWTH TREE DESCRIPTION ]
Describe each ingrowth tree. A carriage
return <CR> will enter a default value of
zero (0).
```

```
TREE # 1
```

```
Tree Species Code (Required-Integer) ---> 202
Diameter at Breast Height (Required-Real) ---> 1.5
Height in feet [>4.5'] (Strongly Recommended-Real) ---> 4.9
Crown Ratio (Strongly Recommended-Real) ---> .8
Number of trees per acre this tree represents (Required) ---> 46
User 2-digit thinning code (Optional-Integer) ---> <CR>
  Spec: 202
  DBH: 1.5
  HT: 4.9
  CR: .80
  EXP: 46.0
  USER: 0      Save this tree (Y)? <CR>
```

```
Another tree (Y)? N
```

```
Do you wish to save the ingrowth data on a file (N)? <CR>
  1 TREE ADDED TO STAND: TEST PLOT
<CR> to continue ...
```

If the resulting data is to be saved, then answer yes to the last question and ORGANON will then request a name to be used for the file.

c. Output

Ingrowth trees are listed separately during trial management reports and plots. After accepting ingrowth management (PM), the ingrowth trees are included in the appropriate diameter class as shown below in a cut report. Not accepting trial management (VM) removes all ingrowth trees from the stand (see TRIAL VS ACCEPTED MANAGEMENT). The following example shows the addition of ingrowth trees after the four thinnings described on pages 85 - 89 have been added to the proposed management scheme.

CUT PER ACRE STAND TABLE EXAMPLE

TEST PLOT			[ 10-21-2011 12:47 PM ]			Page 1		
TRIAL CUT PER ACRE STAND TABLE AT 41 YEARS FOR ALL SPECIES								
DIAM CLASS	RESIDUAL			REMOVAL			CF VOL	SCRIB VOL
	TREES/ ACRE	BA	CF VOL	TREES/ ACRE	BA	CF VOL		
INGROWTH	46.0	.6	2.	0.	.0	.0	0.	0.
0 - 2"	32.8	.1	1.	0.	21.2	.1	1.	0.
2 - 4"	.0	.0	0.	0.	.0	.0	0.	0.
4 - 6"	86.9	11.5	159.	260.	179.2	23.7	326.	520.
6 - 8"	14.8	4.1	71.	213.	27.8	7.6	133.	400.
8 - 10"	10.5	5.0	101.	227.	17.9	8.5	173.	388.
10 - 12"	7.7	5.3	104.	210.	13.1	9.0	177.	360.
12 - 14"	.0	.0	0.	0.	30.1	28.4	615.	1512.
TOTALS	198.6	26.6	439.	910.	289.3	77.2	1426.	3180.

## 2. Overstory Removal (OS)

This routine is used to remove the overstory of two storied stands. As a result, this routine should only be applied to stands where both stories are even-aged.

Application of an overstory removal with a **LIMIT ON MAX. BA** set to **Yes** on the **RUN DEFAULTS** will result in the size-density trajectory being reset to the understory stand at the time of the overstory removal.

To run this routine will require the lower DBH that defines the overstory. The routine also allows the retention of some overstory trees as green trees. This option requires the user to define the lower DBH for defining the green trees and the number of green trees per acre that should remain after overstory removal.

The following is an example where no green trees will be retained after overstory removal:

### OVERSTORY REMOVAL WITHOUT GREEN TREE RETENTION EXAMPLE

Manage ---> **OR**

OVERSTORY REMOVAL Should Only Be applied to Two Storied Stands  
Where Both Stories Are Even-aged

Enter Lower DBH That Defines the Overstory---->**18.0**

Do You Wish to Retain Overstory Green Trees (N) ? ---> **N**

Accept this overstory removal (Y) ? ---> **Y**

The following is an example where ten green trees per acre will be retained after overstory removal:

OVERSTORY REMOVAL WITH GREEN TREE RETENTION EXAMPLE

Manage ---> **OR**

OVERSTORY REMOVAL Should Only Be applied to Two Storied Stands  
Where Both Stories Are Even-aged

Enter Lower DBH That Defines the Overstory---->**18.0**

Do You Wish to Retain Overstory Green Trees (N) ? ---> **Y**

Enter Lower DBH Limit for Overstory Green Trees---->**24.0**

There Are 36.4 Green Trees per Acre with DBH=> 24.0

How Many Green Trees per Acre Should Remain After Overstory Removal?--> **10.0**

Accept this overstory removal (Y) ? ---> **Y**

### 3. **Fertilization (FE)**

Selecting this routine from the management menu allows the fertilization of the stand under the following conditions: (1) a maximum of 400 pounds per acre of nitrogen can be applied at any one time, (2) the stand must have at least 80 percent of its basal area in Douglas-fir, and (3) the stand must be even-aged and under 70 years old. The routine will not allow fertilization if these conditions are not met. The following is an example of the fertilization option:

#### FERTILIZATION EXAMPLE

Manage ---> **FE**

Fertilization has the following restrictions:

1. A maximum of 400 lbs nitrogen per acre can be applied
2. The stand must have at least 80 percent of its basal area in Douglas-fir
3. The stand must be even-aged and under 70 years old

Do you wish to fertilize the stand under these restrictions? -- (N) **Y**

Enter Number of Pounds of Nitrogen per Acre to be Applied----> 200.

#### 4. **Even-age Harvest (EH)**

When you choose an even-age harvest, all remaining trees in the stand, regardless of species, are cut. The only selections available from the main menu after a final harvest are CUT REPORTS and RESTART. The cuts are included on the YIELD TABLE, if requested, and the CUMULATIVE CUT LOG TABLE. The following is an example of selecting an Even-age Harvest option.

EVEN-AGE HARVEST EXAMPLE

```
MANAGE ---> EH
```

```
[ EVEN-AGE HARVEST ]  
*** PLEASE NOTE ***  
HARVEST RESULTS IN ALL TREES TO  
CUT TABLE & NO FURTHER STAND GROWTH !  
From MANAGEMENT MENU, accept final harvest  
with 'PM' -- reject harvest with '<CR>'  
[ <CR> - To Management Menu ]  
<CR> to continue...
```

```
MANAGE ---> PM
```

```
Selected management executing...  
[ please wait -- Cumulative Cut Log Table being calculated ]  
<CR> to continue...
```

## 5. **Pruning (PR)**

There are several approaches you can use to prune trees in a stand. The pruning option can be invoked multiple times from the management menu. Therefore, you can use any combination of these pruning methods to obtain the desired results. After you select a pruning option, you can change your mind and not prune the trees if you chose. In addition, ORGANON lets you cancel your action and returns you to the main menu.

Criteria that can be used to specify a pruning treatment include:

- a.Species or species group to be pruned;
- b.Users code for trees to be pruned;
- c.Minimum DBH for pruned trees;
- d.Whether the target lift height of pruning will be specified by a target crown ratio (as a proportion) or a target crown length (in feet);
- e.Maximum lift height for pruned trees.

All sample trees meeting the pruning criteria will be pruned. Therefore, the number of trees per acre pruned is determined by the sum of the per acre expansion factors for the sample trees selected for pruning.

As a warning, thinnings conducted after pruning could remove pruned trees. Currently, the only method available to "protect" pruned trees is to apply the Users Code thinning option in subsequent thinnings.

This pruning option is a first approximation of pruning effects based upon the manipulation of height-to-crown-base (and therefore crown ratio) of the sample trees and the resulting effects upon diameter growth, height growth and mortality rates of the pruned trees. This approach was taken because of the dearth of pruning data in the Pacific Northwest. Therefore, the predicted effects upon stand development should be viewed as reasonable hypotheses that will be tested when the data from new pruning studies become available.

The following example shows the procedure for pruning all Douglas-fir trees in the stand with a minimum DBH of 3.5-inches, to a target crown ratio of 0.25 and to a maximum lift height of 32.0-feet.

PRUNING EXAMPLE #1

MANAGE ---> **PR**

SPECIES OR SPECIES GROUP DESIRED (AL) ---> **DF**

Enter Users Code for Pruned Trees (<CR>=No Users Code) ---> **<CR>**

Enter Minimum DBH for Pruned Trees (<CR>=Prune all DBHs) ---> **3.5**

[ TARGET HEIGHT OF PRUNING ]

CR - Prune to a Specified Crown Ratio  
CL - Prune to a Specified Crown Length

--- > **CR**

Enter Target Crown Ratio ---> **0.25**

Enter Maximum Lift Height for Pruned Trees (<CR>= No Maximum) ---> **32.0**

17 DF Sample Trees Targeted for Pruning

Accept This Pruning (Y)? ---> **Y**

The following example shows the procedure for pruning all conifer trees in the stand with a users code of 23, to a target crown length of 10.0-feet.

PRUNING EXAMPLE #2

MANAGE ---> **PR**

SPECIES OR SPECIES GROUP DESIRED (AL) ---> **AC**

Enter Users Code for Pruned Trees (<CR>=No Users Code) ---> **23**

Enter Minimum DBH for Pruned Trees (<CR>=Prune all DBHs) ---> <CR>

[ TARGET HEIGHT OF PRUNING ]

CR - Prune to a Specified Crown Ratio  
CL - Prune to a Specified Crown Length

--- > **CL**

Enter Target Crown Length ---> **10.0**

Enter Maximum Lift Height for Pruned Trees (<CR>= No Maximum) ---> <CR>

9 AC Sample Trees Targeted for Pruning

Accept This Pruning (Y) ? ---> **Y**

## **6. Uneven-age Harvest (UH)**

The uneven-age harvest option requires the specification of a target species or species group and a target diameter distribution. The target diameter distribution represents the desired number of trees per acre by two-inch diameter classes, with the 2" diameter class representing trees with dbh's of 0.1" through 2.0", the 4" diameter class representing trees with dbh's of 2.1" through 4.0", etc. The target diameter distribution can be entered either directly or computed from a target q-value.

### **a. Input Directly (ID)**

The target diameter distribution can be input directly into ORGANON either by using an existing file or by entering the data through the keyboard.

#### **1. Existing File Input**

An existing ingrowth file can be created by using either a word processor or by first entering the trees through the keyboard in ORGANON and then saving the file.

You can use any word processor that generates an ASCII file to create the data file. An ASCII file is a file that contains no formatting characters (word wrap, formatting, etc.). This is generally referred to as a flat, or non-document file. Wordstar, WordPerfect, PC-Write, IBM Personal Editor and MS-DOS Line Editor (EDLIN) or Editor can create this type of file. Check your word processor manual for instructions on creating an ASCII file.

Use one line (all characters up to a carriage return) to enter the data for one diameter class. The total number of lines in the file should equal the total number of diameter classes being entered.

Both data elements should be right justified in their field. In the following description, an integer refers to a whole number (no decimal point, i.e., 24). A real number implies a decimal number (i.e., 27.4).

Element	Col #	Comment
1	1-3	Diameter Class Index (INTEGER). A diameter class index of 1 represents trees with dbh's of 0.1" through 2.0", a diameter class index of 2 represents trees with dbh's of 2.1" through 4.0", etc.
2	5-10	Number of Trees per Acre for the Diameter Class Index (REAL-1 decimal place). (e.g., 27.5)

The following example shows the procedure for adding ingrowth trees to a stand using an existing ingrowth file called '**TDIA1**'.

UNEVEN-AGE HARVEST EXAMPLE #1	
MANAGE ---> <b>UH</b>	
SPECIES OR SPECIES GROUP DESIRED (AL) ---> <b>AC</b> <div style="border: 1px solid black; padding: 5px; margin-top: 10px;"> [ TARGET DIAMETER DISTRIBUTION ]                       ID - Input Directly                       CQ - Compute From Q-Value                       NO - No Uneven-age Harvest         </div>	
--- > <b>ID</b>	
Do you wish to use an existing target diameter distribution file (N) ? <b>Y</b> Enter file name for target diameter distribution ---> <b>TDIA1</b> Accept this uneven-age harvest (Y) ? ---> <b>Y</b>	

## 2. Keyboard Input

The following example shows the procedure for creating a target diameter distribution by entering the data through the keyboard.

UNEVEN-AGE HARVEST EXAMPLE #2	
MANAGE ---> <b>UH</b>	
 <b>SPECIES OR SPECIES GROUP DESIRED (AL) ---&gt; <b>AC</b></b>	
[ TARGET DIAMETER DISTRIBUTION ]	
ID - Input Directly CQ - Compute From Q-Value NO - No Uneven-age Harvest	
--- > <b>ID</b>	
 Do you wish to use an existing target diameter distribution file (N)? <b>N</b> Enter max. DBH (nearest even inch) for target dia. distribution ---> <b>24</b>	
 For the .1 to 2.0-inch diameter class Enter the target number of trees per acre ---> <b>100.0</b>	
For the .1 to 2.0-inch diameter class Target number of trees per acre = 100.0 Save this value (Y)? <b>Y</b>	
 For the 2.1 to 4.0-inch diameter class Enter the target number of trees per acre ---> <b>80.0</b>	
For the 2.1 to 4.0-inch diameter class Target number of trees per acre = 80.0 Save this value (Y)? <b>Y</b>	

The above screens are repeated for all of the remaining 12 two-inch diameter classes. This data is then saved on file 'TDIA2' using the following.

```
Do wish to you save the target diameter distribution data on a file (N) ? Y
Enter file name for target diameter distribution data
---> TDIA2
Accept this uneven-age harvest (Y) ? ---> Y
```

b. Compute From Q-Value (CQ)

As an option, the target diameter distribution can be computed from a given q-value. If  $N_i$  is the number of trees per acre in the  $i$ -th diameter class, then  $q$  can be represented by:

$$q = N_{i-1}/N_i$$

The q-value must be greater than 1.0 to generate the reverse-J shape diameter distribution that is normally associated with uneven-age management.

In addition to the q-value, the user must enter the maximum dbh, to the nearest even inch, for the target diameter distribution and the number of trees per acre in the largest diameter class. The latter can be entered directly, or it can be computed from either total number of trees per acre or total basal area per acre for the target diameter distribution using the formulas found in Davis and Johnson (1987).

In the following example, the maximum dbh is 24-inches, the q-value is 1.25, and the number of trees in the largest diameter class is entered directly.

UNEVEN-AGE HARVEST EXAMPLE #3

```
MANAGE ---> UH
```

SPECIES OR SPECIES GROUP DESIRED (AL) ---> **AC**

[ TARGET DIAMETER DISTRIBUTION ]

ID - Input Directly  
CQ - Compute From Q-Value  
NO - No Uneven-age Harvest

--- > **CQ**

Enter max. DBH (nearest even inch) for target dia. distribution ---> **24**

Enter Q-value for the target diameter distribution ---> **1.25**

Number of trees per acre in the largest diameter class will be ...

1. Entered directly
2. Computed from targeted total number of trees per acre
3. Computed from targeted total basal area per acre

ENTER 1, 2 or 3 ---> **1**

Enter trees per acre for the largest dia. class ---> **10.0**

Do wish to you save the target diameter distribution data on a file (N) ? **Y**

Enter file name for target diameter distribution data

---> **TDIA3**

Accept this uneven-age harvest (Y) ? ---> **Y**

#### **d. Thin**

There are several approaches you can use to thin a stand. You can use any combination of these thinning methods to obtain the desired results. All thinning operations are reflected on YIELD TABLES, if requested, and on CUMULATIVE CUT LOG TABLES. After you select each thinning operation, you can change your mind and not thin the stand if you so choose. ORGANON lets you cancel your action and returns you to the main menu.

Thinnings are accomplished with ORGANON by reducing the expansion factors of the trees affected. As an example, a Diameter Proportional thinning is accomplished by reducing the expansion factors of all trees by the fractional value (a constant) needed to meet the user-specified goal. Thinning from above (or below) starts with the largest (or smallest) diameter and sets it and each succeeding smaller (or larger) tree to zero until doing so to the next smaller (larger) tree would remove too many trees per acre. A fractional part of that tree's expansion is then removed to meet your desired goal.

## 1. **Diameter Thin (DB)**

You can choose a diameter thin to thin by diameter class. ORGANON prompts you for the following information:

Species - The species or species group to which the thinning will be applied.

Lower DBH - The smallest diameter for the thinning. This diameter will NOT be included in the thinning.

Percent removal - The percent to remove at the lower diameter.

Upper DBH - The largest diameter for the thinning. This diameter WILL be included in the thinning.

Percent removal - The percent to remove at the largest diameter.

The removal percentages for diameters between the smallest and largest diameters are determined by linear interpolation. The formula for this interpolation is:

$$P_i = [(D_i - D_L) / (D_U - D_L)] [P_U - P_L] + P_L$$

Where,

$P_i$  = Percent removal for an interim diameter

$D_i$  = The interim diameter

$D_L$  = The smallest diameter

$D_U$  = The largest diameter

$P_U$  = Percent removal for the largest diameter

$P_L$  = Percent removal for the smallest diameter

In the following example, a thin of 50% from 2.5" trees linearly decreasing to 10% from 28" trees is performed on the DOUGLAS FIR in the stand.

DIAMETER CLASS THIN EXAMPLE	
MANAGE ---> <b>DB</b>	
SPECIES OR SPECIES GROUP DESIRED (AL) ---> <b>DF</b>	
[ *** WARNING *** ]	
Lower DBH value 'not' included... Upper DBH value included... (i.e. lower < CUT <= upper)	
Enter lower DBH ---> <b>2.5</b> Enter lower removal % ---> <b>50</b> Enter upper DBH ---> <b>28</b> Enter upper removal % ---> <b>10</b>	
Accept this thin (Y) ? ---> <b>&lt;CR&gt;</b>	

## 2. **Basal Area Thin (BA)**

You can choose a basal area thin to remove a certain amount of basal area from the stand. ORGANON first prompts you for the species or species group to which the basal area thin will be applied. The total amount of basal area in the species group you selected will then be displayed on the screen. ORGANON prompts you for the basal area amount to remain after cutting. The basal area cut can be performed from above, below or proportionally across the diameter classes.

In the following example, ORGANON prompts you for a basal area thin. The user selects a thin from above with 42.8 square feet of basal area in DOUGLAS FIR to remain after cut.

BASAL AREA THIN EXAMPLE

MANAGE ---> <b>BA</b>			
<p>SPECIES OR SPECIES GROUP DESIRED (AL) ---&gt; <b>DF</b></p> <p>Basal Area control:</p> <table border="1"><tr><td>A - from above</td></tr><tr><td>B - from below</td></tr><tr><td>P - proportional</td></tr></table> <p>Enter BA Control ---&gt; <b>A</b> Total Basal Area = 63.3 sq. ft. for DOUGLAS FIR Enter basal area sq.ft. to remain after cut ---&gt; 42.8 20.5 sq. ft. basal area to cut ...</p> <p>Accept this thin (Y)? ---&gt; &lt;CR&gt;</p>	A - from above	B - from below	P - proportional
A - from above			
B - from below			
P - proportional			

### 3. **Stand Density Index Thin (DI)**

The current value for Reineke's stand density index is displayed. ORGANON then prompts you for the desired target stand density index. This target stand density index can be achieved by cuts from above, cuts from below, or by proportional cuts. ORGANON attempts to reach the specified target stand density index, although in some circumstances, that target can only be approached. Another thinning attempt, using the same target except from below instead of above (or vice versa), usually achieves an exact target stand density index. In the following example, a user selects a proportional stand density index thinning to a target SDI of 75.0.

STAND DENSITY INDEX THIN EXAMPLE

MANAGE ---> <b>DI</b>			
<p>Stand Density Index control:</p> <table border="1"><tr><td>A - from above</td></tr><tr><td>B - from below</td></tr><tr><td>P - proportional</td></tr></table> <p>Enter SDI control from ---&gt; <b>P</b></p> <p>Stand Density Index is currently: 99. Target SDI ? ---&gt; <b>75.</b></p> <p>Accept this thin (Y) ? ---&gt; <b>&lt;CR&gt;</b></p>	A - from above	B - from below	P - proportional
A - from above			
B - from below			
P - proportional			

#### 4. **User Code Thin (US)**

As defined previously, a numeric user code (with a value between 1 and 99) is a variable that you can enter for each tree record that can later be used in thinning. When you select 'US', ORGANON prompts you for the user code along with the percent of that user code to thin. In the following example, 20 percent of all trees with a user code of 0 are to be cut.

USER CODE THIN EXAMPLE

MANAGE ---> <b>US</b>
Enter user code to thin ---> <b>0</b> Enter percent to cut ---> <b>20</b> Accept this thin (Y)? ---> <b>Y</b>

### **e. Management Reports (RR or CR)**

Reports are available during management in order to view the cumulative effects upon the stand of any management decisions that have been selected (even on a trial basis). During management, RESIDUAL REPORTS (RR) display the stand as it appeared before management. CUT REPORTS (CR) display the cumulative results of all management selections.

### **f. Restart Management (RS)**

Restart terminates the current management selections. The stand is returned to the condition prior to entry into the management routine. The stand is now ready to begin a new management selection. If no new management is desired, choose a Void Management (VM) exit instead of RESTART.

#### RESTART MANAGEMENT EXAMPLE

MANAGE ---> <b>RS</b>
MANAGE --->

## g. Exit Management

### 1. **Void Management (VM)**

After a management option or options have been made on a trial basis, you may view any of the residual or cut reports.

If, at that time, the results of the management are not as desired, you can void all management options, leave the MANAGEMENT MENU, and go back to the MASTER MENU. The stand then remains as it was prior to entering the management selection. Be sure to check this because CUT REPORTS are available only after a cut and they are otherwise unavailable.

The RESIDUAL REPORTS selection displays the stand for confirmation. If the management performed was not desired, but another management attempt will be made, select a RESTART (RS) rather than a Void Management (VM) exit. MANAGEMENT is again available from the master menu.

#### VOID MANAGEMENT EXAMPLE

```
MANAGE ---> VM
MANAGE --->
```

### 2. **Perform Management (PM)**

By selecting PERFORM MANAGEMENT, the management scheme, as previously defined by selections, becomes a permanent action on the stand and all reports reflect that change on a permanent--not trial-- basis. MANAGEMENT will no longer be available from the master menu until after the next growth cycle.

#### PERFORM MANAGEMENT EXAMPLE

```
MANAGE ---> PM
```

```
Selected management executing...
```

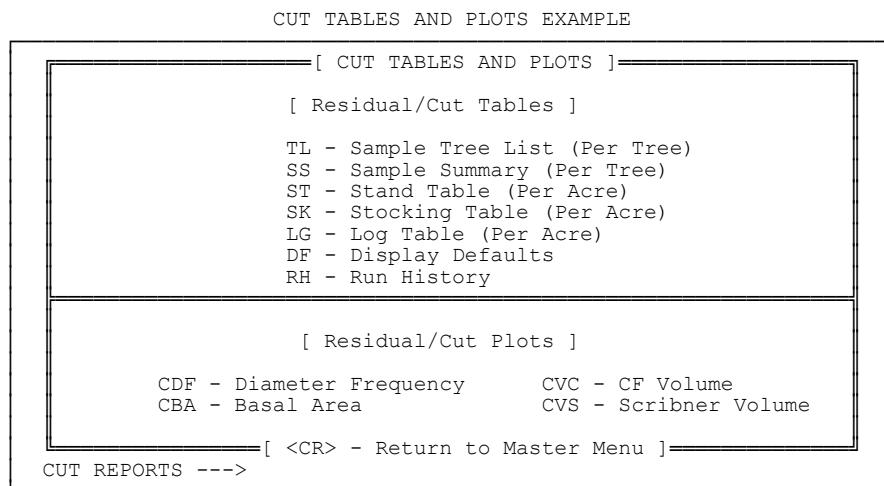
```
[ please wait -- Cumulative Cut Log Table being calculated ]
<CR> to continue...
```

```
ORGANON --->
```

## 5. Cut Tables and Plots (CR)

Cut Reports are only available on the main menu immediately following a management cut. Cut Reports are also available within the Management Menu and reflect any cuts currently requested whether or not those cuts have been accepted (See TRIAL VS ACCEPTED MANAGEMENT). All cut tables and plots except the Cut Log Table show both residuals and removals in one table or plot. The Cut Log Table is a log table of the cut trees only.

The following example shows the reports and plots available from the CUT REPORTS MENU.



### a. Sample Tree List (TL)

The Cut Sample Tree List is very similar to the Residual Sample Tree List. It provides a listing of those sample trees with expansion factors greater than zero (i.e., trees still living).

### b. Sample Summary (SS)

The Cut Sample Summary is very similar to the Residual Sample summary. It provides the per tree average attributes for the residual sample trees.

### c. Per Acre Stand Table (ST)

The Cut Stand Table is somewhat similar to the Residual Stand Table. The difference is that the left side of the Cut Stand Table is labeled 'RESIDUAL', and provides by 2" diameter class, the number of trees, basal area, cubic foot volume and scribner volume per acre for the stand after cutting. The right side of the Cut Stand Table, labeled 'REMOVAL', provides the same information as the left for the cut trees. Values for each diameter class displayed in the tables include the upper diameter but not the lower diameter.

The following is an example of a Cut Stand Table after performing a basal area thin from above with 85.1 square feet to remain after cut (See BASAL AREA THIN).

CUT STAND TABLE EXAMPLE

TEST PLOT		[ 10-21-2011 8:49 AM ]				Page 1			
POST CUT PER ACRE STAND TABLE AT 41 YEARS FOR ALL SPECIES									
		RESIDUAL						REMOVAL	
DIAM CLASS		TREES/ ACRE	CF BA	SCRIB VOL	TREES/ ACRE	CF BA	SCRIB VOL		
0 - 2"		56.9	.3	2.	0.	.0	.0	0.	0.
2 - 4"		.0	.0	0.	0.	.0	.0	0.	0.
4 - 6"		271.2	36.9	493.	782.	.0	.0	0.	0.
6 - 8"		28.6	6.9	117.	367.	.0	.0	0.	0.
8 - 10"		42.9	18.6	366.	860.	.0	.0	0.	0.
10 - 12"		20.8	14.5	283.	571.	.0	.0	0.	0.
12 - 14"		9.9	8.4	167.	361.	20.3	20.0	452.	1277.
TOTALS		430.3	85.1	1428.	2991.	20.3	20.0	452.	1277.

## d. Stocking Table (SK)

The Cut Stocking Table is similar to the Residual Stocking Table, except that the left side of the Cut Stocking Table is labeled 'RESIDUAL'. The Cut Stocking table provides by species group, the number of trees, basal area, cubic foot volume and scribner volume per acre for the stand after cutting. The right side of the table, labeled 'REMOVAL', provides the same information as the left for the cut trees. The following is an example of a Stocking Table after performing a basal area thin from above with 85.1 square feet to remain after cut (See BASAL AREA THIN).

### CUT STOCKING TABLE EXAMPLE

(POST) C U T S T O C K T A B L E										
TEST PLOT				[ 10-21-2011 8:50 AM ]						
SPECIES		AT	TREES/	CF	SCRIB	TREES/	CF	SCRIB	VOL	
SPECIES		YR	ACRE	BA	VOL	ACRE	BA	VOL	VOL	
Doug Fir	41		430.3	85.1	1428.	2941.	20.3	20.0	451.9	1276.9
TOTALS:			430.3	85.1	1428.	2941.	20.3	20.0	451.9	1277.
Stand Density Index: 191.					Relative Density Index: .360					
Quadratic Mean Diameter: 6.0					Height of 40 Largest: 55.0					
Mean Diameter: 5.4					Mean Crown Ratio: .780					

## e. Log Table (LG)

The Cut Log Table provides the same information as the Residual Log Table except for cut trees. Values for each diameter class displayed in the tables include the upper diameter but not the lower diameter. The following is an example of a Log Table after performing a basal area thin from above with 85.1 square feet to remain after cut (See BASAL AREA THIN).

CUT LOG TABLE EXAMPLE

CUT LOG TABLE (TOTAL 41 YEARS)						
TEST PLOT		[ 10-21-2011 8:40 AM ]				
LOG LENGTH: 32 feet		MIN LOG LENGTH: 8.0 feet		TOP DIAM: 4.0 inches		
Top Diameter		Doug Fir Logs	G/W Fir Logs	P/S Pine Logs	Other Conifer Logs	Vol
4 - 6"		14.2	153.3	.0	.0	.0
6 - 8"		20.3	1123.6	.0	.0	.0
TOTALS						
Logs:		34.5		.0	.0	.0
Volumes:		1276.9		.0	.0	.0
AVG VOLUME:		37.0		.0	.0	.0

## f. Display Defaults (DF)

The Display Defaults on the CUT REPORTS MENU is the same as the Display Defaults on the RESIDUAL REPORTS MENU.

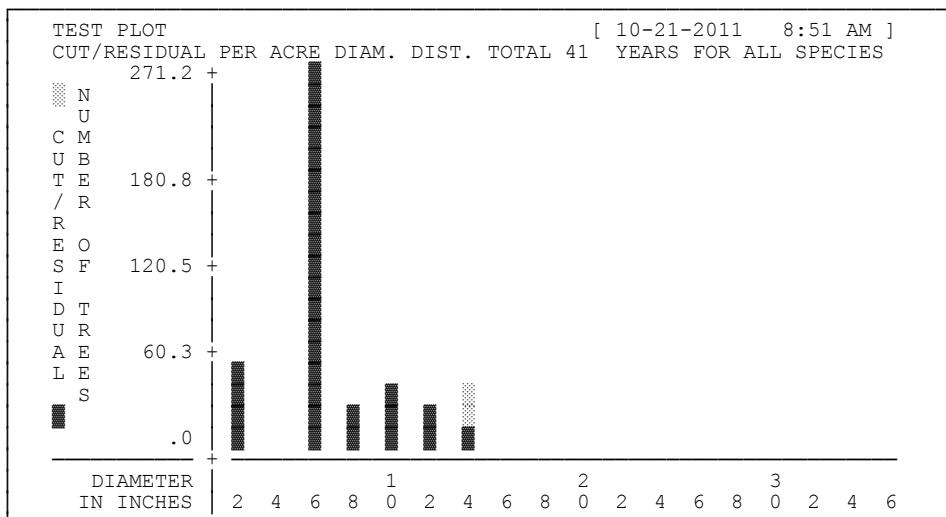
## g. Run History (RH)

The Run History on the CUT REPORTS MENU is the same as the Run History on the RESIDUAL REPORTS MENU.

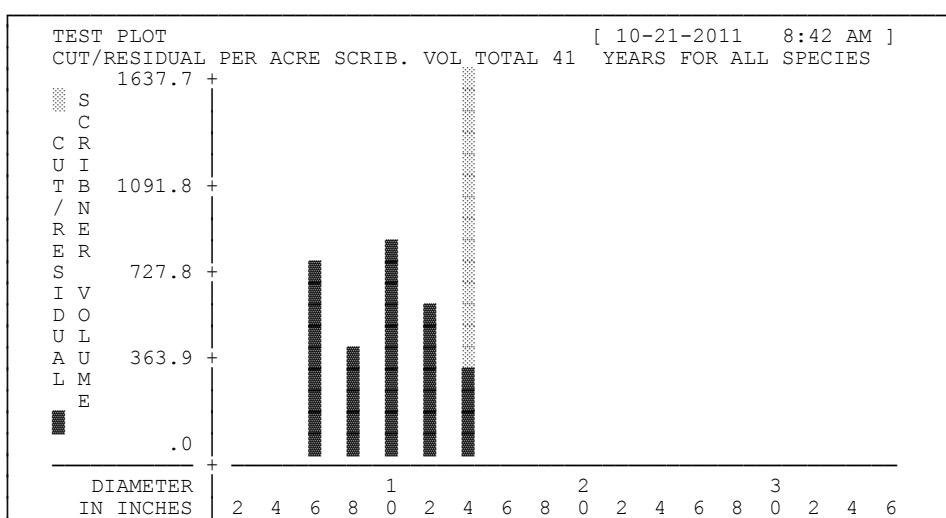
## h. Plots

The following two cut histograms, Diameter Frequency (CDF) and Scribner Volume (CVS), show the same total amount in each diameter class as the corresponding residual histogram. The two plotting symbols distinguish between the after-cut residual on the bottom and the cut portion on the top. The diameter values displayed on the X-axis indicate the upper diameter of the class (i.e., 14 represents 12" < DBH ≤ 14").

CDF PLOT EXAMPLE



CVS PLOT EXAMPLE



## 6. Restart ORGANON (RS)

When you select RESTART from the main menu, all output is saved from the current model run, if requested. ORGANON then re-initializes and begins from the point of entering a file name of a previously edited data file. In the following example, ORGANON is restarted, the yield table is saved but cumulative cut log table is not saved. A new data file, called PLOT356, is then selected for the next analysis.

### RESTART ORGANON EXAMPLE

```
ORGANON ---> RS
```

```
Save yield table (N)? ---> Y
Save cumulative cut log table (N)? ---> <CR>
```

```
Enter tree data file name [NO extension (i.e. A:MYFILE) ] ---> PLOT356
```

## 7. Quit (QU)

When an ORGANON run ends, you must choose QUIT or RESTART to properly close all files associated with that run.

### ORGANON QUIT EXAMPLE

```
ORGANON ---> QU
[ please wait -- yield table transfer is proceeding ]
[ please wait -- cumulative cut log table transfer is proceeding ]
[ ALL OUTPUT HAS BEEN WRITTEN TO FILE: TESTOUT ]

Stop - Program terminated.
C:\>
```

## VII. EXAMPLE OF FINAL OUTPUT FILE

After QUIT (QU) or RESTART (RS), the output file is closed and consists of all stand parameters, calibrations, program defaults, tables and plots previously requested for file output along with the yield table, if requested. A cumulative cut log table follows the yield table. The final report in the output file will be a run history which is the same as the Run History available during program execution in the CUT REPORT and RESIDUAL REPORT MENUS. This report represents the final run history. Each growth request will be listed with stand age and number of cycles, each management option will be itemized as to type and species, and each fertilization will include age and quantity. You should request plots and tables during program execution to save in an output file as well as to display on the screen. In this way, the stand description, defaults, and run history are associated with the reports requested.

An output listing of sample file TESTPLOT follows. The stand is grown one cycle. All species are proportionally thinned to 20 square feet basal area, and all species are also thinned 20% for all user codes of 0. The stand is grown for two more cycles then clear cut.

O R G A N O N  
ORegon Growth ANalysis and projection system  
Growth & Yield Project for  
Southwest Oregon Mixed Conifer Forests

SW OREGON VERSION, EDITION 8.0  
by David W. Hann  
and Mark L. Hanus  
Department of Forest Management  
Oregon State University

This model was funded by:  
Forestry Intensified Research (FIR) and USDI BLM  
[ 10-21-2011 8:39 AM ]

Tree Data File: TESTPLOT  
Stand Identification: TEST PLOT  
Number of Plots/Points: 4  
Number of Sample (obs.) Trees: 19

EXPANSION FACTORS WERE SET AS FOLLOWS:  
SUBSAMPLE 1 ---> FIXED 7.8 ft. radius  
SUBSAMPLE 2 ---> FIXED 15.6 ft. radius  
SUBSAMPLE 3 ---> VARIABLE BAF = 20.0

Douglas Fir Site Index = 109.4  
Ponderosa Pine Site Index = 102.9  
Breast height stand age = 28  
Total stand age - 36

--> --> --> --> --> W A R N I N G <-- <-- <-- <-- <--  
50 SAMPLE TREES IS THE MINIMUM RECOMMENDED !!!  
--> --> --> --> W A R N I N G <-- <-- <-- <-- <--

Run Defaults:

1. TRIPLING: No
2. DISPLAY MENUS: Yes
3. USE HEIGHT CALIB: Yes
4. USE HTCB CALIB: Yes
5. USE DIAM. GRO CALIB: Yes
6. LIMIT ON MAX. SDI: Yes
7. WOOD QUALITY OUTPUT: No
8. JUVENILE WOOD CORE: Age
9. PRINTER FORM FEED: No
10. TREE LIST OUTPUT: No
11. VOLUME EQUATIONS: OSU

Board Foot Defaults:

12. LOG TOP DIAM: 4. inches
13. TRIM ALLOWANCE: 8. inches
14. STUMP HEIGHT: .5 feet
15. LOG LENGTH: 32 feet
16. MIN LOG LENGTH: 8.0 feet

Cubic Foot Defaults:

17. TOP DIAM (0.0"-6.0"): 0. inches
18. STUMP HT: .0 feet

CALIBRATION RATIOS USED FOR THIS RUN:

	HEIGHT/DIAM	HTCB	DIAM
DOUGLAS FIR	.70	1.23	1.00
GRAND/WHITE FIR	1.00	1.00	1.00
PONDEROSA PINE	1.00	1.00	1.00
SUGAR PINE	1.00	1.00	1.00
INCENSE CEDAR	1.00	1.00	1.00
WESTERN HEMLOCK	1.00	1.00	1.00
REDCEDAR	1.00	1.00	1.00
PACIFIC YEW	1.00	1.00	1.00
MADRONE	1.00	1.00	1.00
CHINKAPIN	1.00	1.00	1.00
TANOAK	1.00	1.00	1.00
CANYON LIVE OAK	1.00	1.00	1.00
BIG LEAF MAPLE	1.00	1.00	1.00
ORE. WHITE OAK	1.00	1.00	1.00
CAL. BLACK OAK	1.00	1.00	1.00
RED ALDER	1.00	1.00	1.00
PACIFIC DOGWOOD	1.00	1.00	1.00
WILLOW	1.00	1.00	1.00

DIAMETER GROWTH RATE GENETIC WORTH (%) = 0.0

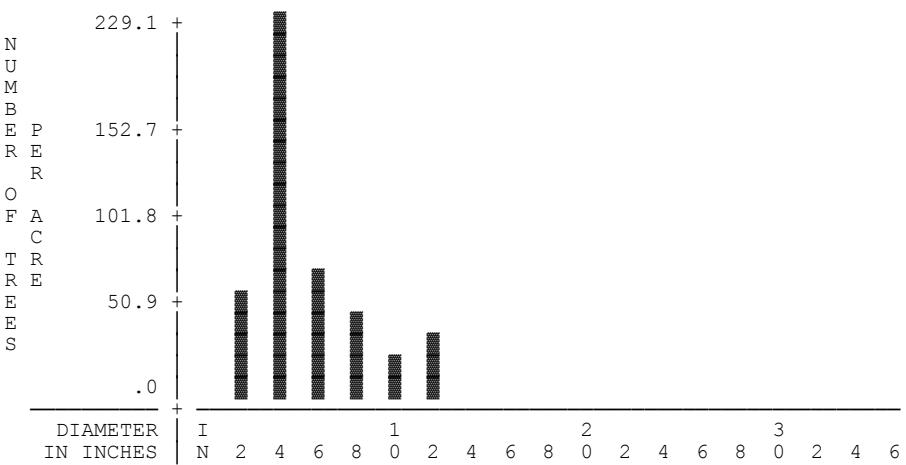
HEIGHT GROWTH RATE GENETIC WORTH (%) = 0.0

SWISS NEEDLE CAST FOLIAGE RETENTION VALUE = 7.00

TEST PLOT [ 10-21-2011 8:46 AM ] Page 1  
INITIAL PER ACRE STAND TABLE AT 36 YEARS FOR ALL SPECIES

DIAM CLASS	E N D I N G				NET 0-YEAR CHANGE			
	TREES/ ACRE	CF BA	SCRIB VOL	TREES/ ACRE	CF BA	SCRIB VOL		
0 - 2"	57.3	.0	0.	0.				
2 - 4"	229.1	15.0	142.	0.				
4 - 6"	71.6	8.4	112.	0.				
6 - 8"	43.0	12.4	197.	571.				
8 - 10"	20.9	10.0	158.	357.				
10 - 12"	30.2	20.0	362.	701.				
TOTALS	451.9	65.8	970.	1628.				

TEST PLOT [ 10-21-2005 8:46 AM ]  
PER ACRE DIAM. DIST. TOTAL 36 YEARS FOR ALL SPECIES



TEST PLOT  
PER ACRE STAND TABLE AT

[ 10-21-2011 8:47 AM ]

Page 1

DIAM CLASS	E N D I N G				NET				5-YEAR CHANGE			
	TREES/ ACRE	CF BA	SCRIB VOL	TREES/ ACRE	CF BA	SCRIB VOL	TREES/ ACRE	CF BA	SCRIB VOL	TREES/ ACRE	CF BA	SCRIB VOL
0 - 2"	53.9	.2	2.	0.	-3.4	.2	2.	0.				
2 - 4"	.0	.0	0.	0.	-229.1	-15.0	-142.	0.				
4 - 6"	266.1	35.2	485.	780.	194.6	26.8	373.	780.				
6 - 8"	42.5	11.6	204.	613.	-0.4	-0.7	8.	42.				
8 - 10"	28.4	13.4	275.	615.	7.6	3.4	117.	258.				
10 - 12"	20.8	14.4	281.	570.	-9.4	-5.6	-80.	-131.				
12 - 14"	30.1	28.4	615.	1512.	30.1	28.4	615.	1512.				
TOTALS	441.9	103.2	1862.	4090.	-10.0	37.5	892.	2462.				

Y I E L D T A B L E S

TEST PLOT  
DATA FILE: TESTPLOT

[ 10-21-2005 8:42 AM ]

SPECIES	AT YR	TREES/ ACRE				CF BA				SCRIB VOL			
		TREES/ ACRE	CF BA	SCRIB VOL	TREES/ ACRE	CF BA	SCRIB VOL	TREES/ ACRE	CF BA	SCRIB VOL			

ENDING			R E S I D U A L			Y I E L D			0-YR CHANGE		
Doug Fir	36	451.9	65.8	970.	1628.						

TOTAL:	451.9	65.8	970.	1628.							
TOTAL MAI:		27.		45.							
CONIFER MAI:		27.		45.							
QUADRATIC MEAN DIAMETER:		5.2			RELATIVE DENSITY INDEX:		.295				
ESTIMATED % CROWN CLOSURE:		68.0			HEIGHT OF 40 LARGEST:		48.7				

ENDING			R E S I D U A L			Y I E L D			5-YR CHANGE		
Doug Fir	41	441.9	103.2	1862.	4090.	-10.0	37.5	892.1	2461.8		

TOTAL:	441.9	103.2	1862.	4090.	-10.0	37.5	892.1	2462.		
MORTALITY: Conifers					10.0	0.6	7.4	7.		
TOTAL MAI:		45.		100.		PAI:	178.4	492.		
CONIFER MAI:		45.		100.		PAI:	178.4	492.		
QUADRATIC MEAN DIAMETER:		6.5			RELATIVE DENSITY INDEX:		.422			
ESTIMATED % CROWN CLOSURE:		76.1			HEIGHT OF 40 LARGEST:		60.6			

RESIDUAL			C U T			Y I E L D			REMOVAL		
Doug Fir	41	198.6	26.6	439.	910.	289.3	77.2	1425.8	3180.1		

TOTAL:	198.6	26.6	439.	910.	289.3	77.2	1425.8	3180.		
QUADRATIC MEAN DIAMETER:		5.0			RELATIVE DENSITY INDEX:		.121			
ESTIMATED % CROWN CLOSURE:		35.5			HEIGHT OF 40 LARGEST:		48.2			

ENDING			R E S I D U A L			Y I E L D			5-YR CHANGE		
Doug Fir	46	194.8	49.7	902.	2514.	-3.8	23.1	462.7	1604.1		

TOTAL:	194.8	49.7	902.	2514.	-3.8	23.1	462.7	1604.		
MORTALITY: Conifers					3.8	0.2	3.1	5.		
TOTAL MAI:		51.		124.		PAI:	92.5	321.		
CONIFER MAI:		51.		124.		PAI:	92.5	321.		
QUADRATIC MEAN DIAMETER:		6.8			RELATIVE DENSITY INDEX:		.200			
ESTIMATED % CROWN CLOSURE:		47.5			HEIGHT OF 40 LARGEST:		56.7			

ENDING			R E S I D U A L			Y I E L D			5-YR CHANGE		
Doug Fir	51	191.6	72.2	1517.	4241.	-3.2	22.6	614.7	1727.3		

TOTAL:	191.6	72.2	1517.	4241.	-3.2	22.6	614.7	1727.		
MORTALITY: Conifers					3.2	0.4	5.7	15.		
TOTAL MAI:		58.		146.		PAI:	122.9	345.		
CONIFER MAI:		58.		146.		PAI:	122.9	345.		
QUADRATIC MEAN DIAMETER:		8.3			RELATIVE DENSITY INDEX:		.269			
ESTIMATED % CROWN CLOSURE:		55.2			HEIGHT OF 40 LARGEST:		66.3			

## YIELD TABLES

TEST PLOT

DATA FILE: TESTPLOT

Page 2

[ 10-21-2011 8:42 AM ]

SPECIES	AT YR	TREES/ACRE			CF VOL			SCRIB/ACRE			TREES/ACRE			CF VOL			SCRIB/VOL		
		BA	VOL	CF VOL	BA	VOL	CF VOL	BA	VOL	CF VOL	BA	VOL	CF VOL	BA	VOL				

ENDING				RESIDUAL				YIELD				5-YR CHANGE			
--------	--	--	--	----------	--	--	--	-------	--	--	--	-------------	--	--	--

Doug Fir	56	188.5	95.1	2301.	7069.	-3.2	22.9	784.3	2827.5						
----------	----	-------	------	-------	-------	------	------	-------	--------	--	--	--	--	--	--

TOTAL:	188.5	95.1	2301.	7069.	-3.2	22.9	784.3	2828.
--------	-------	------	-------	-------	------	------	-------	-------

MORTALITY: Conifers					3.2	0.6	9.8	24.
---------------------	--	--	--	--	-----	-----	-----	-----

TOTAL MAI:	67.	183.			PAI:	156.9	566.
------------	-----	------	--	--	------	-------	------

CONIFER MAI:	67.	183.			PAI:	156.9	566.
--------------	-----	------	--	--	------	-------	------

QUADRATIC MEAN DIAMETER:	9.6				RELATIVE DENSITY INDEX:	.334	
--------------------------	-----	--	--	--	-------------------------	------	--

ESTIMATED % CROWN CLOSURE:	60.6				HEIGHT OF 40 LARGEST:	75.9	
----------------------------	------	--	--	--	-----------------------	------	--

ENDING				RESIDUAL				YIELD				5-YR CHANGE			
--------	--	--	--	----------	--	--	--	-------	--	--	--	-------------	--	--	--

Doug Fir	61	185.3	118.2	3247.	11590.	-3.1	23.4	946.3	4521.1						
----------	----	-------	-------	-------	--------	------	------	-------	--------	--	--	--	--	--	--

TOTAL:	185.3	118.2	3247.	11590.	-3.1	23.4	946.3	4521.
--------	-------	-------	-------	--------	------	------	-------	-------

MORTALITY: Conifers					3.1	0.8	15.6	42.
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TOTAL MAI:	77.	242.			PAI:	189.3	904.
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CONIFER MAI:	77.	242.			PAI:	189.3	904.
--------------	-----	------	--	--	------	-------	------

QUADRATIC MEAN DIAMETER:	10.8				RELATIVE DENSITY INDEX:	.396	
--------------------------	------	--	--	--	-------------------------	------	--

ESTIMATED % CROWN CLOSURE:	64.5				HEIGHT OF 40 LARGEST:	85.7	
----------------------------	------	--	--	--	-----------------------	------	--

ENDING				RESIDUAL				YIELD				5-YR CHANGE			
--------	--	--	--	----------	--	--	--	-------	--	--	--	-------------	--	--	--

Doug Fir	66	182.0	141.0	4329.	16436.	-3.3	22.8	1081.5	4846.2						
----------	----	-------	-------	-------	--------	------	------	--------	--------	--	--	--	--	--	--

TOTAL:	182.0	141.0	4329.	16436.	-3.3	22.8	1081.5	4846.
--------	-------	-------	-------	--------	------	------	--------	-------

MORTALITY: Conifers					3.3	1.0	23.4	81.
---------------------	--	--	--	--	-----	-----	------	-----

TOTAL MAI:	87.	297.			PAI:	216.3	969.
------------	-----	------	--	--	------	-------	------

CONIFER MAI:	87.	297.			PAI:	216.3	969.
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QUADRATIC MEAN DIAMETER:	11.9				RELATIVE DENSITY INDEX:	.459	
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ESTIMATED % CROWN CLOSURE:	67.3				HEIGHT OF 40 LARGEST:	95.0	
----------------------------	------	--	--	--	-----------------------	------	--

RESIDUAL				FINAL				HARVEST				REMOVAL			
----------	--	--	--	-------	--	--	--	---------	--	--	--	---------	--	--	--

Doug Fir	66	.0	.0	0.	0.	0.1	182.0	141.0	4328.7	16436.2					
----------	----	----	----	----	----	-----	-------	-------	--------	---------	--	--	--	--	--

TOTAL:	.0	.0	0.	0.	182.0	141.0	4328.7	16436.
--------	----	----	----	----	-------	-------	--------	--------

QUADRATIC MEAN DIAMETER:	.0				RELATIVE DENSITY INDEX:	.000	
--------------------------	----	--	--	--	-------------------------	------	--

ESTIMATED % CROWN CLOSURE:	.0				HEIGHT OF 40 LARGEST:	.0	
----------------------------	----	--	--	--	-----------------------	----	--

## CUMULATIVE CUT LOG TABLE

[ 10-21-2005 8:42 AM ]

TEST PLOT

LOG LENGTH: 32 feet

MIN LOG LENGTH: 8.0 feet

TOP DIAM: 4.0 inches

Top Diameter	Doug Fir Logs	G/W Fir Logs	P/S Logs	Pine Vol	Other Conifer Logs	Conifer Vol
--------------	---------------	--------------	----------	----------	--------------------	-------------

6 -- 8"	341.1	5323.6	.0	.0	.0	.0	.0
---------	-------	--------	----	----	----	----	----

6 -- 8"	62.3	3514.5	.0	.0	.0	.0	.0
---------	------	--------	----	----	----	----	----

8 -- 10"	62.1	5154.4	.0	.0	.0	.0	.0
----------	------	--------	----	----	----	----	----

10 -- 12"	14.5	1874.6	.0	.0	.0	.0	.0
-----------	------	--------	----	----	----	----	----

12 -- 14"	10.3	1810.4	.0	.0	.0	.0	.0
-----------	------	--------	----	----	----	----	----

14 -- 16"	7.7	1938.7	.0	.0	.0	.0	.0
-----------	-----	--------	----	----	----	----	----

## TOTALS

Logs:	497.9	.0	.0	.0	.0	.0
-------	-------	----	----	----	----	----

Volumes:	19616.3	.0	.0	.0	.0	.0
----------	---------	----	----	----	----	----

AVG VOLUME:	39.4	.0	.0	.0	.0	.0
-------------	------	----	----	----	----	----

RUN HISTORY

```
*****  
YEAR          ACTIVITY  
*****  
36          GROWTH --> 1 CYCLE  
41          THIN DBH (DF) 2.5 " --> 50 % 28 " -->10 %  
41          THIN BA (DF) from above --> 42.8 resid. sq ft  
41          SDI THIN proportional --> Target 75  
41          THIN USER CODE = 0 --> 20 %  
41          INGROWTH (46 TPA - DOUGLAS FIR)  
41          GROWTH --> 5 CYCLES  
66          EVEN-AGE HARVEST
```

## VIII. FORMAT FOR WOOD QUALITY OUTPUT FILE

### Line 1 - Tree and Stand Attributes at Time of Cutting or Pruning

1. Tree Species	I4,8X
2. Tree DBH	F10.4
3. Tree Total Height	F10.4
4. Tree Crown Ratio	F10.4
5. Tree Expansion Factor	F10.4
6. Stand Breast Height Age	I4
7. Number of Branches (NB <sub>i</sub> ) Records for ith Tree	I4
8. Total Stand Age or Elapsed Time	I4
9. Number of Prunings (NP <sub>i</sub> ) for ith Tree	I4

### If NP<sub>i</sub>>0, Then Lines 2... (NP<sub>i</sub>+1)

1. Total Stand Age or Elapsed Time of Pruning	I4
2. Tree DBH at Time of Pruning	F10.4
3. Tree Total Height at Time of Pruning	F10.4
4. Tree Crown Ratio at Time of Pruning	F10.4
5. Tree Expansion Factor at Time of Pruning	F10.4
6. Lift Height of Pruning for Tree	F10.4

### If NP<sub>i</sub>=0, Then Lines 2 ... (NB<sub>i</sub>+1);

### If NP<sub>i</sub>>0, Then Lines (NP<sub>i</sub>+1) ... (NP<sub>i</sub>+NB<sub>i</sub>+1)

1. Height to Branch	I6 (F6.1)
2. Largest Branch Diameter	I6 (F6.2)
3. Diameter of the Juvenile Wood Core at Branch	I6 (F6.2)
4. Diameter Inside Bark at Branch	I6 (F6.2)

### Line S(NP<sub>i</sub>+NB<sub>i</sub>+1)+1

-999 I4

### Line S(NP<sub>i</sub>+NB<sub>i</sub>+1)+2

1. File Name for Yield Table Output	A40
2. Year of Run	I3
3. Month of Run	I3
4. Day of Run	I3
5. Hour of Run	I3
6. Minute of Run	I3
7. Second of Run	I3

### Lines S(NP<sub>i</sub>+NB<sub>i</sub>+1)+3 .... Contain The Run's History

1. Total Age or Elapse Time	3X,I3
2. Description of Activity	10X,A49

#### DESCRIPTIONS OF ACTIVITIES

The following are the first six characters in the description of each activity and the activity they describe in the Run History:

<u>First Six Characters</u>	<u>Activity</u>
EVEN-A	The Stand was Clearcut
FERTIL	The Stand was Fertilized
GROWTH	The Stand was Grown
INGROW	Ingrowth was Added to the Stand
OR CUT	The Overstory was Removed from the Stand
PRUNE	Trees in the Stand were Pruned
THIN B	The Stand was Thinned to a Target Basal Area
THIN D	The Stand was Thinned by DBH Classes
THIN S	The Stand was Thinned to a Target SDI
THIN U	The Stand was Thinned by User Codes
UNEVEN	Stand was Cut to a Target Diameter Distribution

## IX. SUPPLEMENTARY PROGRAM 'PLTYLD'

Supplementary program named 'PLTYLD' has been designed to read an ORGANON output file containing a yield table and generate plots of specified yield table variables over stand age (for even-age stands) or elapsed time (for uneven-age stands). You need only provide an ORGANON output file name (including drive designator, if necessary) and the plots desired. The following yield table variables may be plotted:

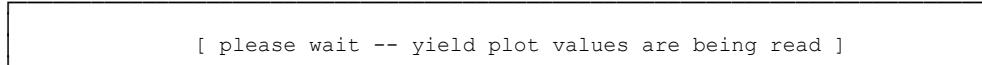
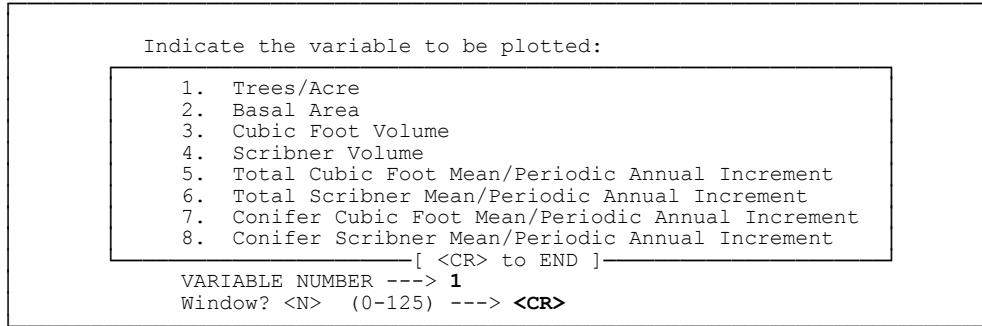
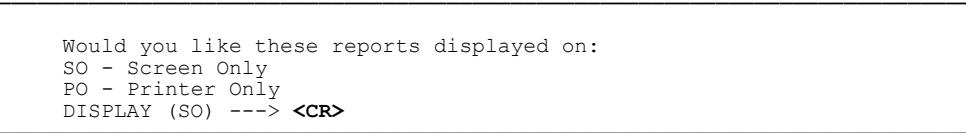
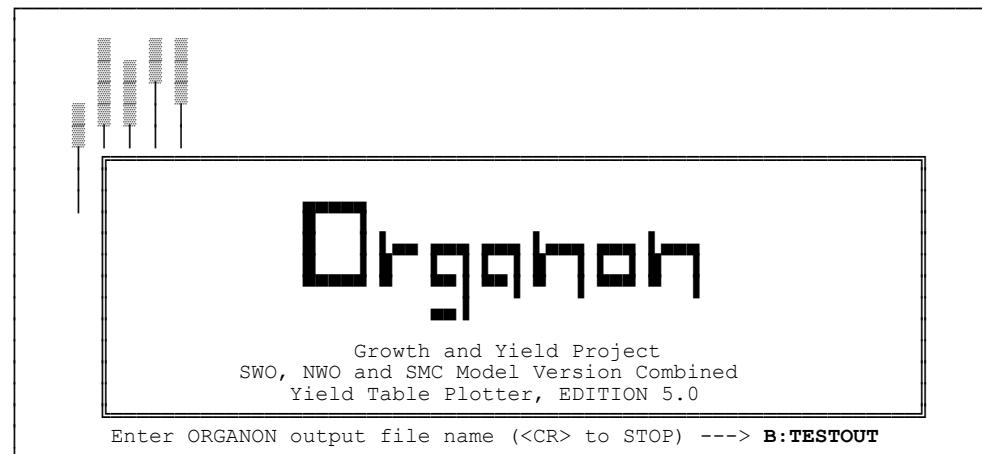
```
ntrees per acre
nbasal area per acre
n cubic foot volume per acre
n Scribner volume per acre
ntotal cubic foot mean/periodic annual increment
ntotal Scribner mean/periodic annual increment
nconifer cubic foot mean/periodic annual increment
nconifer Scribner mean/periodic annual increment
```

The 'PLTYLD' program can also be used to create a comma delineated ASCII file in which each row contains the following stand attributes: total stand age, total number of trees per acre, total basal area per acre, total cubic foot volume per acre and total board foot volume per acre. This file can then be imported into a spreadsheet program for additional analysis and graphing capabilities.

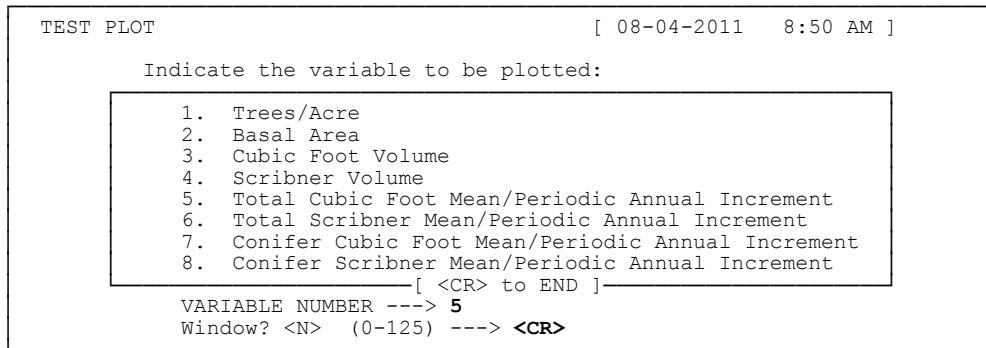
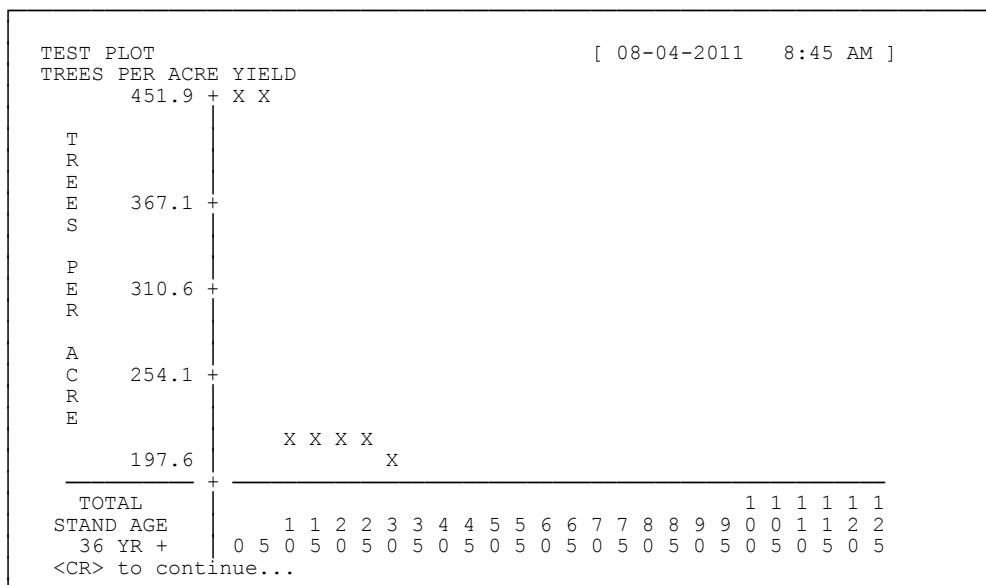
Display destination (Screen or Printer ONLY) and plot windows must be selected for these plots in the same manner as for display of CUT or RESIDUAL REPORTS described earlier in the main ORGANON program. The following example displays screens showing a plot of Trees Per Acre and Total Cubic Foot Mean/Periodic Annual Increment.

'PLTYLD' EXAMPLE

C:> **PLTYLD**

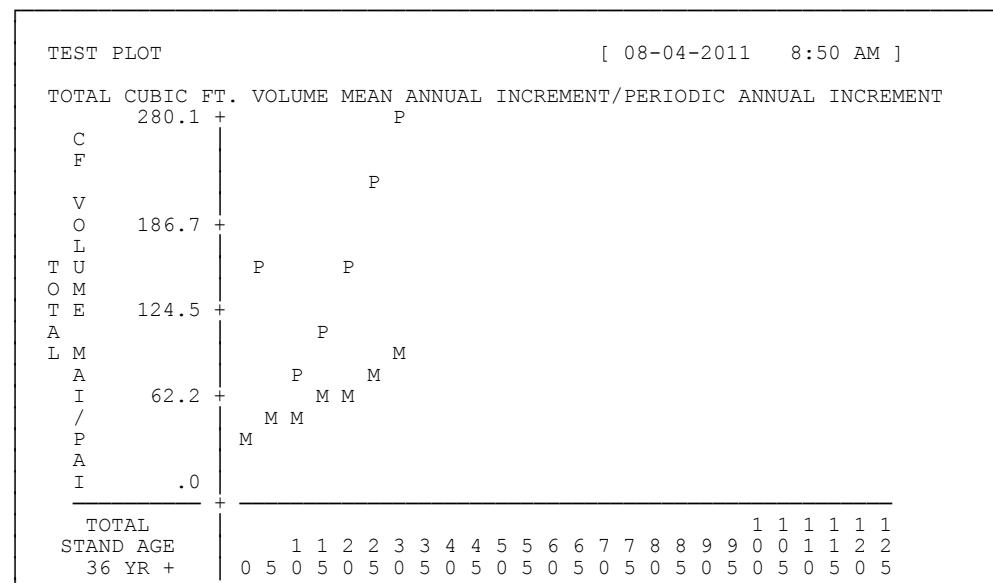


'PLTYLD' EXAMPLE (continued)



[ please wait -- yield plot values are being read ]

'PLTYLD' EXAMPLE (continued)



Indicate the variable to be plotted:

- 1. Trees/Acre
- 2. Basal Area
- 3. Cubic Foot Volume
- 4. Scribner Volume
- 5. Total Cubic Foot Mean/Periodic Annual Increment
- 6. Total Scribner Mean/Periodic Annual Increment
- 7. Conifer Cubic Foot Mean/Periodic Annual Increment
- 8. Conifer Scribner Mean/Periodic Annual Increment

VARIABLE NUMBER ---> **<CR>**

Do you wish to output an ASCII file of the yield data (N) ? **Y**  
Enter name for ASCII file ---> **B:TESTOUT.ASC**

Enter ORGANON output file name (<CR> to STOP) ---> **<CR>**  
Stop - Program terminated.

## X. FORMAT FOR TREE LIST OUTPUT FILE

The tree list output file contains stand level information on the first line, followed NTREES times (NCYCLE + 1) lines with tree information on each line, where NTREES is the number of input trees and NCYCLE is the number of growth cycles. The data items on each line are separated by commas.

### Line 1 - Initial Stand Attributes

1. Twenty character stand identification
2. Breast height age for the stand (0 if uneven-aged) if SWO-ORGANON, NWO-ORGANON, or SMC-ORGANON, and total age if RAP-ORGANON.
3. Douglas-fir site index if SWO-ORGANON, NWO-ORGANON, or SMC-ORGANON, and red alder site index if RAP-ORGANON.
4. Ponderosa pine site index if SWO-ORGANON, western hemlock site index if NWO-ORGANON or SMC-ORGANON, and Douglas-fir site index if RAP-ORGANON.

### Lines 2 to {[NTREES x (NCYCLE +1)] + 1}

1. Growth cycle
2. Point number
3. Tree number
4. Species
5. User code
6. DBH either initially or at the end of the growth period
7. Total tree height either initially or at the end of the growth period
8. Crown ratio either initially or at the end of the growth period
9. Number of trees per acre expansion factor either initially or at the end of the growth period
10. Number of trees per acre dying in the growth period
11. Number of trees per acre cut in the growth period
12. Cubic foot volume for the tree's DBH, total height and crown ratio
13. Scribner board foot volume for the tree's DBH, total height and crown ratio

## XI. WARNING AND ERROR MESSAGES

ORGANON may display error or warning messages during program execution. The following list describes the messages that ORGANON issues to a user should problems occur during program execution. The interpretations of warning and error messages should clarify their meaning so you can maintain your work flow with ORGANON.

MESSAGE	MEANING
All errors have NOT been corrected. ORGANON cannot be run.	After exit from the correction module, there are still tree data errors that have not been corrected. Re-entry to the corrector module will occur until all errors are corrected.
ALL OUTPUT HAS BEEN WRITTEN TO FILE: xxxx	At the end of an ORGANON run or at the point of a restart request, the yield table is written to the end of the designated output file shown in quotes. Following the yield table is a history of the completed ORGANON run.
xxx crown ratios predicted from yyy entered crown ratios	During raw data file entry, crown ratios were predicted for xxx trees with missing crown ratios by equation and calibration ratio determined by yyy trees with entered crown ratios for the same species.
*** DBH=0.0 FOR TREE xxxx IS NOT VALID	An illegal tree diameter of 0. has been read from the input file.
*** ERROR -- NO TREES LEFT	When in the correction module, all tree records have been designated to be deleted.
*** ERROR -- ONLY xxxx RECORDS WERE ENTERED	During tree data correction, the tree record number specified to edit was greater than the number of trees entered.
*** ERROR--REENTER --->	The user-requested input has been rejected. This can happen when: <ol style="list-style-type: none"> <li>1. A real number has been entered when an integer is requested</li> <li>2. A character has been entered when a numeric value has been requested</li> <li>3. Some character other than YES, yes, NO or no has been entered when a Yes/No answer was requested</li> <li>4. A invalid character has been entered for a requested character.</li> <li>5. A numeric value does not fall within the requested range</li> </ol>
*** ERROR--SPECIES CODE 0 INVALID	When entering a data set through the setup module, if a species is not entered or is entered as a zero the user is asked "Is a point with no trees?" If no, then a code must be entered.
*** ERROR INCOMPLETE TREE	In the correction module, a point with no trees must have at least a point number before exit from the correction module is allowed.

continued

MESSAGE	MEANING
*** ERROR--REENTER SPECIES --->	In the correction module, if a species is not entered, the user is asked "Is this a point with no trees?" If no, then a species code must be entered
*** ERROR--REENTER (0 <= YR <= 125 and divisible by 5) --->	In the window option of PLTYLD, the user specified minimum and maximum years must fall between 0 and 125 and they must be divisible by 5.
FILE 'ORGANON.DEF' DOES NOT EXIST!	During default selection, a request was made to use the preset user defaults in file ORGANON.DEF on the default drive. This file does not exist at this time and selection <3> should be used to create this file.
FILE 'xxx' DOES NOT EXIST! (Drive OK?)	When a file name for an existing file is requested in ORGANON, the file name entered did not exist on the specified drive. If a drive was not specified, the file did not exist on the default drive. Be sure to enter the drive specification or check the spelling of the file name. Data files must have no extensions.
FILE 'xxx' DOES NOT EXIST! Either re-enter a data file name (check DRIVE) or enter <CR> to STOP	When a ORGANON output file name is re-requested in PLTYLD, the file name entered did not exist on the specified drive. If a drive was not specified, the file did not exist on the default drive. Be sure to enter the drive specification or check the spelling of the file name. A carriage return will indicate no more output files to plot.
FILE 'xxx' EXISTS! -- OVERWRITE? (Y)	When an output or wood quality file is requested, a check is made to see if the file name entered already exists. If it does, a check is made to see if it should be overwritten. This check is also made during the creation of a batch file.
*** HEIGHT <= 4.5' FOR TREE xxxx IS NOT VALID	Heights entered from the input data file must be greater than 4.5 feet.
*** ILLEGAL PLOT/POINT NUMBER OR BLANK LINE FOR TREE xxxx *** RECORD WILL BE IGNORED ***	A blank line has been read from the input data file or the plot/point number is an illegal 0.
*** ILLEGAL SPECIES CODE xxx FOR TREE yyyy	A species code read from the input file is not one of the legal species codes listed in the SPECIES CODE NUMBER section.
Maximum number of trees (2000) reached.	When adding trees during ingrowth management, the tree list has reached 2000 and no more ingrowth trees may be added.
NO GROWTH CYCLES POSSIBLE -- ALL TREES HARVESTED	No more growth cycles can be requested as all trees have been harvested by accumulated thins or a FINAL HARVEST had been conducted on the stand.
NO GROWTH CYCLES POSSIBLE -- NO REMAINING MAJOR SPECIES	No more growth cycles are possible as all of the major tree species have been cut.

continued

MESSAGE	MEANING
No species in that group...	During reports or management, a species is selected for display or management. This message will appear if the species does not exist or no longer exists because of previous management selections.
Not enough species in that group...	In a plot during initial data entry, a calibration plot has been requested for a species in which there were not enough entries to determine a calibration other than 1.0.
ORGANON will calculate	In the corrector module, a missing variable was specified that ORGANON will compute during the data completion step following. This will include expansion factors and heights only.
*** please wait - xxxxxxxxxxxxxxxxxx	ORGANON is busy calculating, reading or writing and the model will not resume execution until this action is completed.
QUESTIONABLE MERCHANTABLE HEIGHT!!!	During calculations of log volume from taper equations, merchantable tree height has been determined to be negative or greater than the total tree height.
*** STAND IDENTIFICATION 'xxxxxxxxxxxxxxx' *** ONLY FIRST 20 CHARACTERS WILL BE USED.	Stand identification title can only be 20 characters long. Only the first 20 characters of the identification will be used. All remaining characters are truncated.
SYSTEM OVERFLOW...MUST BE REPORTED	This message can only occur if the TRIPLING option has been selected. If this message occurs, please report all related stand information to Dept. of Forest Resources, College of Forestry, Oregon State University
The following are the data scan results... Errors MUST be corrected before model is run.	After the raw data file is input, a list of invalid or missing elements is listed. Invalid elements must be corrected before further model execution.
The maximum number of trees has been exceeded. Program execution is terminated.	A maximum of 2000 trees can be input from the data input file. Reduce size of input file by reducing the number of sample plots taken in the stand. This can be done by dividing the stand into several smaller stands or by randomly eliminating sampling plots.
THERE WERE NO MAJOR TREE SPECIES (DF, WF, GF, PP, SP, IC) ENTERED. THIS DATA FILE CANNOT BE ACCEPTED BY ORGANON	All data sets input to ORGANON must contain trees from the six major species groups.
xxx tree heights predicted from xxx entered	During raw data file entry, tree heights were determined for xxx trees with missing heights by equation and calibration ratio determined by trees with entered heights in same species.
xxx tree records have been read...	xxx trees have been read into the main ORGANON module from the '.INP' file.
*** UNACCEPTABLE xx SITE INDEX VALUE***	Unacceptable DF or PP site index value has been input. DF and PP site index cannot be less than 44.5 or greater than 164.5.

continued

MESSAGE	MEANING
--> --> W A R N I N G <-- <-- DOUGLAS FIR SITE INDEX IS OUTSIDE THE RANGE USED TO BUILD ORGANON !!!	Douglas Fir site index must be in the range from 55.5 to 120.5, the range of the sampling set used to build the ORGANON model.
--> --> W A R N I N G <-- <-- 50 SAMPLE TREES IS THE MINIMUM RECOMMENDED!!!	Fifty trees is the minimum recommended number of trees to sample.
--> --> W A R N I N G <-- <-- MINIMUM AGE FOR A STAND IS 15 YEARS !!!	An even age stand must be a minimum age of 15 years.
*** WARNING *** Negative potential height growth set to 0 !!	During a growth cycle, the height growth of a tree has been calculated to be negative. The height growth will be set to 0 and the growth cycle will continue. This error will occur if the tree is taller than the maximum potential the tree could achieve for the stand's site index. To eliminate this problem, the user should consider increasing the stand's site index.
WARNING -- POINT xx HAS NO TREES	During data input, a valid point number has been read with all remaining fields blank or 0. This indicates a plot/point with no trees.
> > > > W A R N I N G > > > > *** MAXIMUM CROWN WIDTH OF TREE xx IS OUT OF RANGE DBH=xxx HEIGHT=xxx MAXIMUM CROWN WIDTH = xxx	During data completion or diameter growth, a maximum crown width for the specified tree was calculated and determined to be less than or equal to or greater than or equal to 100 using the equations of Paine and Hann (1982).
> > > > W A R N I N G > > > > DF/GF/WF/SP SITE INDEX MAY BE INCORRECTLY ESTIMATED. GROWTH MODEL MAY NOT WORK CORRECTLY.	Douglas Fir site index does not correspond to DF/WF/GF/SP tree heights entered.
> > > > W A R N I N G > > > INCENSE-CEDAR SITE INDEX MAY BE INCORRECTLY ESTIMATED. GROWTH MODEL MAY NOT WORK CORRECTLY.	Incense Cedar site index determined from the Douglas Fir site index does not correspond to the incense cedar tree heights entered.
--> --> W A R N I N G <-- <-- PONDEROSA PINE SITE INDEX IS OUTSIDE THE RANGE USED TO BUILD ORGANON !!!	Ponderosa Pine site index must be in the range from 60 to 125, the range of the sampling set used to build the ORGANON model.
> > > > W A R N I N G > > > PONDEROSA PINE SITE INDEX MAY BE INCORRECTLY ESTIMATED. GROWTH MODEL MAY NOT WORK CORRECTLY.	Ponderosa Pine site index does not correspond to Ponderosa Pine tree heights entered.
--> --> W A R N I N G <-- <-- STAND IS OUTSIDE LIMITS OF SPECIES MIX USED TO BUILD ORGANON!!!	If stand age is less than or equal to 40 years, at least 60% of the stand basal area must be in the major species. If the stand age is greater than 40 years, at least 80% of the stand basal area must be in the major species.
*** WARNING *** ALL MAJOR SPECIES HAVE BEEN CUT NO MORE GROWTH WILL BE POSSIBLE	No more growth cycles are possible as all of the major tree species have been cut.
*** WARNING *** Lower DBH value 'not' included ... Upper DBH value included ... (i.e., lower < cut <= upper)	In diameter thin (DB), trees with dbh's equal to the lower dbh value will not be removed in thinning while trees with dbh's equal to the upper dbh value will be removed in thinning.

continued

MESSAGE	MEANING
----- W A R N I N G ----- A MAJORITY OF THE STAND IS OVER 120 YEARS BH AGE!!! FUTURE PREDICTIONS ARE EXTRAPOLATIONS!!!	The upper BH age for the sampling set used to build the ORGANON model was 120 years. Therefore, predictions for BH ages above 120 years are extrapolations of the model.

## XII. LITERATURE CITED

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